

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 2, 2004, 16:16:51 ; Search time 56 Seconds  
(without alignments)  
1635.451 Million cell updates/sec

Title: US-09-915-515a-1

Perfect score: 2998  
Sequence: 1 MDRVSGVALENDERAKNT.....IVPLVEILKNDGVREARSG 577

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database :

1: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1980.DAT:\*  
2: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1981.DAT:\*  
3: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1982.DAT:\*  
4: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1983.DAT:\*  
5: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1984.DAT:\*  
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10: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1989.DAT:\*  
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12: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1991.DAT:\*  
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21: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2000.DAT:\*  
22: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:\*  
23: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:\*  
24: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2003.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2998	100.0	577	23 AA014442	Protein of Newcastle
2	2993	99.8	577	18 AA018228	Paramyxovirus haem
3	2985	99.6	577	8 AAP70843	Sequence of Newcas
4	2920	97.4	577	14 AAR39703	Haemagglutinin-neu
5	2920	97.4	577	16 AAR80558	Newcastle's disease
6	2920	97.4	577	17 AAM06827	Newcastle disease
7	2920	97.4	577	21 AAY51232	Newcastle disease
8	2915	97.2	581	15 AAR58559	Newcastle Disease
9	2915	97.2	581	15 AAR58559	Newcastle disease

10	2915	97.2	581	18 AAM10690	Newcastle disease
11	2915	97.2	581	20 AAY21982	Seq ID No: 13 of U
12	2915	97.2	581	21 AAB36038	Protein encoded by
13	2915	97.2	581	21 AAY58182	NDV haemagglutinin
14	2847	95.0	616	10 AAP6147	Sequence of Newcas
15	2839	94.7	616	11 AAR06329	Newcastle disease
16	2742	91.5	571	19 AAM44940	Newcastle disease
17	2735	91.2	568	19 AAM62989	HN protein of Newc
18	2727	91.0	568	17 AAM03551	Newcastle disease
19	2727	91.0	568	17 AAM03138	Newcastle disease
20	2727	91.0	568	17 AAM03325	Newcastle disease
21	2727	91.0	568	19 AAM49683	Newcastle disease
22	2679	89.4	571	10 AAP91960	Haemagglutinin and
23	2390	79.7	453	18 AAP81829	Paramyxovirus solu
24	776	25.9	565	24 ABJ18511	Human Cryptovirus
25	773	25.8	582	22 AAB67478	Amino acid sequenc
26	770	25.7	582	22 AAP93666	Haemagglutinin-neu
27	479	16.0	575	23 AAU79234	Sendai virus HN (h
28	449	15.0	572	10 AAP94799	Perdue strain of t
29	449	15.0	572	10 AAP94800	Parainfluenzae-3 g
30	449	15.0	572	14 AAR31957	Sequence encoded b
31	449	15.0	572	16 AAR79037	PI-3 haemagglutini
32	444.5	14.8	572	21 AAB08627	Amino acid sequenc
33	442.5	14.8	572	14 AAR39284	Parainfluenza viru
34	441.5	14.7	572	23 AATU4678	Parainfluenza viru
35	428.5	14.3	572	11 AAR06023	Viral haemagglutin
36	395.5	13.2	558	6 AAP50501	Sequence of bovine
37	205	6.8	36	20 AAB75537	Antigenic site of
38	184	6.1	33	20 AAB75507	Antigenic site of
39	145	4.8	1723	23 AAB94267	Chlamydia pneumoni
40	144	4.8	1723	23 AAB90585	Chlamydia pneumoni
41	144	4.8	1723	23 AAB94266	Chlamydia pneumoni
42	122	4.1	22	20 AAB97457	Antigenic site of
43	119	4.0	881	22 AAG70752	S cerevisiae apopt
44	119	4.0	1198	20 AAT92428	Amino acid sequenc
45	116	3.9	2261	24 ABJ18914	Pathogen specific

#### ALIGNMENTS

RESULT 1	AA014442	standard; protein; 577 AA.
ID	AA014442;	
AC	AA014442;	
XX		
DT	09-MAY-2002	(first entry)
XX		
DE	Protein of Newcastle Disease Virus Haemagglutinin-Neuraminidase.	
XX		
KW	Paramyxovirus haemagglutinin-neuraminidase; HN; x-ray crystallography;	
KW	crystal form; inhibitor; antiinflammatory; virucide; infection; croup;	
KW	bronchitis; pneumonia; respiratory disease; Newcastle disease virus; NDV.	
XX		
OS	Newcastle disease virus.	
XX		
PN	W0200210459-A2.	
XX		
PD	07-FEB-2002.	
XX		
PF	27-JUL-2001; 2001WO-US23623.	
XX		
PR	27-JUL-2000; 2000US-221199P.	
XX		
PA	(BIOC-) BIOCRYST PHARM INC.	
PA	(STUD-) ST JUDE CHILDREN'S RES HOSPITAL.	
PA	(UYSA-) UNIV ST ANDREWS.	
PA	(UYBA-) UNIV BATH.	
XX		
PI	Taylor G, Portner A, Takamoto T, Babu VS, Rowland RS,	
XX		
DR	WPI; 2002-195970/25.	

PT	Identifying paramyxovirus haemagglutinin neuraminidase (HN) inhibitor
PT	useful for treating or preventing croup, by applying three-dimensional
PT	structure of active site of paramyxovirus HN to design or select
PT	inhibitor -
XX	
PS	Claim 1; Page 30; 30pp; English.
XX	
CC	The invention relates to structures of paramyxovirus haemagglutinin-
CC	neuraminidases (HN), as determined by x-ray crystallography, the use of
CC	such structures to solve the structure of paramyxovirus HN homologues,
CC	mutants, co-complexes, and other crystal forms and the use of such
CC	structures, their homologues, mutants, co-complexes, and other crystal
CC	forms, to design inhibitors of paramyxovirus HN. The paramyxovirus HN's
CC	have anti-inflammatory and virocidic activity and can be used for
CC	identifying a potential inhibitor of paramyxovirus HN. The paramyxovirus
CC	HN of the invention useful for treating or preventing undesired
CC	properties of infection by paramyxoviruses, and thus for treating or
CC	preventing croup, bronchitis, pneumonia, or any other respiratory disease
CC	caused by paramyxovirus. This sequence represents the protein of
CC	Newcastle Disease Virus (NDV) Haemagglutinin-Neuraminidase of the
CC	invention.
CC	
XX	
SQ	Sequence 577 AA;
Query Match	100.0%; Score 2998; DB 23; Length 577;
Best Local Similarity	100.0%; Pred. No. 5.5e-283;
Matches 577; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
OY	1 MDRAVSOALNDEEAKNTRLPRIALLLTLYTLTSVASLYSGASTPSPDLVIP 60
Dd	1 MDRVSVALENDEREAQKTRLLPRIALLLTLYTLTSVASLVYSMGASTPSPDLVGIP 60
OY	61 TRISAEKITSALGSNDVDVRIKYVALSEPLALNTETTIMATLSYOINGAANN 120
Dd	61 TRISAEEKITSAUGSNDVDVRIKYVALSEPLALNTETTINMATSLSOINGAANN 120
OY	121 SGWGAPIHDPDTIGIKELIYDNASDVTSFPYPAFOEHNFIPAPTTGSGCTRIPIPFDM 180
Dd	121 SGWGAPIHDPDTIGIKELIYDNASDVTSFYPFAFOEHLNFI PAPTTGSGCTRIPIPFDM 180
OY	181 SATHYCYHANVILSCGRDSSHSHOVLAGVARTTAGTGIIFESTASILDPTONRKKCSV 240
Dd	181 SATHCYHANVILSCGRDSSHSHOVLAVLTAAGTATGRI PSTLSISLDPTONRKKCSV 240
OY	241 SATPLGCDMLCSKVETEEDENSNAPVTLMAGRGAFPGQYHEKDLDTYTLFEDWVANYP 300
Dd	241 SATPLGCDMLCSKVETEEDENSAPVTLMAGRGAFPGQYHEKDLDTYTLFEDWVANYP 300
OY	301 GVGGGSFLIDGRAVPFSVYGGLKENSPSDTVQEGKIYIYRYNDTCPEDDYQIRMAKSSYK 360
Dd	301 GVGGGSFLIDGRAVPFSVYGGLKENSPSDTVQEGKIYIYRYNDTCPEDDYQIRMAKSSYK 360
OY	361 PGRFGRKIRIOQAIIISIXTSLSGEBPVLTVPNTYTLMGABERILLTGTSHTLYRGSSY 420
Dd	361 PGRFGRKIRIOQAIIISIXTSLSGEBPVLTVPNTYTLMGABERILLTVGISHTLYRGSSY 420
OY	421 FSPALLYMYTNSNKATLTPYTFNAFRPGSI PCQASARCNSCVTYGVYDPYLIYYR 480
Dd	421 FSPALLYMYTNSNKATLTPYTFNAFRPGSI PCQASARCNCSVTGYVTDYDYLIIYYR 480
OY	481 NHTLRGVEGTMLDSHOARLNPAASAVFDSTSRIRITRVSSSTKAAYTTSTCEKVVKTNT 540
Dd	481 NHTLRGVEGTMLDSGOARLNPAASAVFDSTSRIRITRVSSSTKAAYTTSTCKVKTKNT 540
OY	541 YCLSTIAEISNTLPFGFRIYVPLIVELTKNDGVREARG 577
Dd	541 YCLSTIAEISNTLPFGFRIYVPLIVELTKNDGVREARG 577
RESULT 2	
ID	AAM18228 standard; Protein; 577 AA.
ID	AAM18228

Query Match	99.8% Score 2993; DB 18; Length 577;	Beet Local Similarity 99.7%; Pred. No. 1.7e-282;	Matches 575; Conservative 1; Mismatches 1; Indels 0; Gaps 0
QY	1 MDRVSVQVLENDEREAQNTWRLIFRIALLLVTLATSVASLVYSGASTPSDLVGP	60	
DB	1 MDRVSVQVLENDEREAQNTWRLIFRIALLLVTLATSVASLVYSGASTPSDLVGP	60	
QY	61 TRISPAEKRTISALGSNOVDVRIKYQVALSSPLALNTETTINNAITSLSQINGAANN	120	
DB	61 TRISPAEKRTISALGSNOVDVRIKYQVALSSPLALNTETTINNAITSLSQINGAANN	120	
QY	121 SGWGAPIHDPPDIGIGKELVVDNADSVTSFSPSAFQSHLNFIPAPTTGSGGCTRI	180	
DB	121 SGWGAPIHDPPDIGIGKELVVDNADSVTSFSPSAFQSHLNFIPAPTTGSGGCTRI	180	
QY	181 SATHYCYTHANVILSGCRDHSRSHOVLAVGAVRTTAQRIIFESTLASISLDDPQNRKSCSV	240	
DB	181 SATHYCYTHANVILSGCRDHSRSHOVLAVGAVRTTAQRIIFESTLASISLDDPQNRKSCSV	240	
QY	241 SATPAGCDMLCSKYETEEDBYNSAVPTLMAGRLGFGQYHEKLDVYTTLEFEDVWVANYP	300	

RESULT 2  
AAW18228  
ID AAW18228 standard; Protein; 577 AA.

Db 181 SATIICYTHINVLISGCRDHSHQVLALGVLRITATGRIFESTLRSISLDDTONKRSQSV 240

Qy 241 SATPLGCDMLCSKYATEBEEDYNASVPTLMAHGRIGFDQYHEKLDVPTLLFEEDVANYP 300

```
Db 211 SATPLGCDMLCSKYTEEBEDYNSAVPTLMAGRLGFDGQYHEKDLVTTTFEDWVANYP 300
Qy 301 GVGGGSFIDGRVWFVSGYGLKPNPSDPTVOEGKYIYKRYNDTCPEDDYQIRMAKSSYK 360
Db 301 GVGGGSFIDGRVWFVSGYGLKPNPSDPTVOEGKYIYKRYNDTCPEDDYQIRMAKSSYK 360
Qy 361 PGRFGKRIQOAILISIKVSTISLGEDPVLTVPPNVTTLMGAEGRILTVGTHFLYORGSSY 420
Db 361 PGRFGKRIQOAILISIKVSTISLGEDPVLTVPPNVTTLMGAEGRILTVGTHFLYORGSSY 420
Qy 421 FSPALLYPMYVSNKTATLHSPYFNATFRPGSIPCOASARCPNCSVTVYDPPYLIFYYR 480
Db 421 FSPALLYPMYVSNKTATLHSPYFNATFRPGSIPCOASARCPNCSVTVYDPPYLIFYYR 480
Qy 481 NHTLRGVFGTMDSEQARLNPASAVFDSTSRSTRIRVSSSTKAYTSTGCKVVKTKNT 540
Db 481 NHTLRGVFGTMDSEQARLNPASAVFDSTSRSTRIRVSSSTKAYTSTGCKVVKTKNT 540
Qy 541 YCLSIABISNTLFGFRIVPLVLEILKNDGVREARSG 577
Db 541 YCLSIABISNTLFGFRIVPLVLEILKNDGVREARSG 577
```

RESULT 3  
AAP70843  
ID AAP70843 standard; protein; 577 AA.

XX AAP70843;  
XX AC  
XX 25-MAR-2003; (updated)  
DT 03-APR-1991 (first entry)  
XX DE  
XX Sequence of Newcastle Disease Virus (NDV) HN polypeptide.

XX Epitope; probe; diagnosis.  
XX OS  
XX Newcastle Disease Virus.

XX EP227414-A.

XX 01-JUL-1987.

XX 16-DEC-1986; 86EP-0309804.

XX 15-JUL-1986; 86US-0885765.

XX 18-DEC-1985; 85GB-0031147.

XX 14-APR-1986; 86GB-0009037.

XX (NATR ) NAT RES DEV CORP.

XX Bingham RW, Chambers P, Emerson PT, Millar NS;

XX WPI; 1987-179630/26.

XX N-PSDB; AAN70261.

XX Newcastle disease virus gene clones - comprise polynucleotide(s)

XX encoding the HN and/or F protein of Newcastle disease virus RNA

XX Example; pages 11-16; 22pp; English.

XX An artificial polynucleotide encoding an HN and/or F polypeptide of

XX Newcastle Disease Virus (NDV) DNA, a bioprecursor of the

XX polypeptide, or an epitopic portion of the polypeptide or an

XX artificial nucleotide complementary to the polynucleotide are

XX claimed. The polynucleotides are useful for preparing a probe for

XX extracting similar genes from a gene library or for identifying the

XX presence of NDV virions in a sample obtd. from poultry.

XX (Updated on 25-MAR-2003 to correct PA field.)

XX Sequence 577 AA;

XX Query Match 99.6%; Score 2985; DB 8; Length 577;

Best Local Similarity 99.5%; Pred. No. 1e-281;  
Matches 574; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

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Qy 1 MDRVSVQVALENDREAKNTWRLFRJAIIILLTVTLATSYASIVSGASTPBDVIGIP 60
Db 1 MDRVSVQVALENDREAKNTWRLFRJAIIILLTVTLATSYASIVSGASTPBDVIGIP 60
Qy 61 TRISRAEKTISALGSNOVDVRIYKQVALESPLALNTEYTNMNAITSLSYQINGAAN 120
Db 61 TRISRAEKTISALGSNOVDVRIYKQVALESPLALNTEYTNMNAITSLSYQINGAAN 120
Qy 121 SGWAPLHDPDFIGIGIKELIVDNASVTSFYPAPQEHNLFIAPPTGSGCTRI 180
Db 121 SGWAPLHDPDFIGIGIKELIVDNASVTSFYPAPQEHNLFIAPPTGSGCTRI 180
Qy 181 SATHYCTHANVILSGCDBSHSHQYALAGVLRRTATGRIFPSTLRSLSDOSQNRKCSV 240
Db 181 SATHYCTHANVILSGCDBSHSHQYALAGVLRRTATGRIFPSTLRSLSDOSQNRKCSV 240
Qy 241 SATPLGCDMLCSKYTEEBEDYNSAVPTLMAGRLGFDGQYHEKDLVTTTFEDWVANYP 300
Db 241 SATPLGCDMLCSKYTEEBEDYNSAVPTLMAGRLGFDGQYHEKDLVTTTFEDWVANYP 300
Qy 301 GVGGGSFIDGRVWFVSGYGLKPNPSDPTVOEGKYIYKRYNDTCPEDDYQIRMAKSSYK 360
Db 301 GVGGGSFIDGRVWFVSGYGLKPNPSDPTVOEGKYIYKRYNDTCPEDDYQIRMAKSSYK 360
Qy 361 PGRFGKRIQOAILISIKVSTISLGEDPVLTVPPNVTTLMGAEGRILTVGTHFLYORGSSY 420
Db 361 PGRFGKRIQOAILISIKVSTISLGEDPVLTVPPNVTTLMGAEGRILTVGTHFLYORGSSY 420
Qy 421 FSPALLYPMYVSNKTATLHSPYFNATFRPGSIPCOASARCPNCSVTVYDPPYLIFYYR 480
Db 421 FSPALLYPMYVSNKTATLHSPYFNATFRPGSIPCOASARCPNCSVTVYDPPYLIFYYR 480
Qy 481 NHTLRGVFGTMDSEQARLNPASAVFDSTSRSTRIRVSSSTKAYTSTGCKVVKTKNT 540
Db 481 NHTLRGVFGTMDSEQARLNPASAVFDSTSRSTRIRVSSSTKAYTSTGCKVVKTKNT 540
Qy 541 YCLSIABISNTLFGFRIVPLVLEILKNDGVREARSG 577
Db 541 YCLSIABISNTLFGFRIVPLVLEILKNDGVREARSG 577
```

RESULT 4  
AAR39703  
ID AAR39703 standard; protein; 577 AA.

XX AAR39703;  
XX AC  
XX 25-MAR-2003 (updated)  
DT 10-JAN-1994 (first entry)

XX Haemagglutinin-neuraminidase of Newcastle disease virus.

XX Homology vector; swinepox virus; recombinant; antigenic peptide;

XX vaccine; ss.

XX Newcastle disease virus.

XX WO9314194-A1.

XX 22-JUL-1993.

XX 13-JAN-1993; 93WO-US00324.

XX 13-JAN-1992; 92US-0820154.

XX (SYTR ) SYNTRO CORP.

XX Cochran MD, Junker DE;

XX WPI; 1993-243210/30.



QY 241 SATPLGCDMLCSKVTETEBEDYNSAVPTLMAHGLGFDGQHEKDLDTVTLLFEDVWVANYP 300  
 DB 241 SATPLGCDMLCSKATETEBEDYNSAVPTLMAHGLGFDGQHEKDLDTVTLLFEDVWVANYP 300  
 QY 301 GVGGSFIDGRVWFVYGLKPNPSDPTVOEGKYIYKRYNDTCDEDDYOIRMAKSSYK 360  
 DB 301 GVGGSFIDGRVWFVYGLKPNPSDPTVOEGKYIYKRYNDTCDEDDYOIRMAKSSYK 360  
 QY 361 GVGGSFIDGRVWFVYGLKPNPSDPTVOEGKYIYKRYNDTCDEDDYOIRMAKSSYK 420  
 DB 361 GVGGSFIDGRVWFVYGLKPNPSDPTVOEGKYIYKRYNDTCDEDDYOIRMAKSSYK 420  
 QY 421 FSPALLYPMYVSNKTATLHSPYTFNAFTPGSIPCOASARCPNSCVTVGYTDPYPLIFR 480  
 DB 421 FSPALLYPMYVSNKTATLHSPYTFNAFTPGSIPCOASARCPNSCVTVGYTDPYPLIFR 480  
 QY 481 NHTLRGVGTMLDSEQARLNPAFAVFDSTSRITRVSSSTKAYTTSTCKVVKTKT 540  
 DB 481 NHTLRGVGTMLDSEQARLNPAFAVFDSTSRITRVSSSTKAYTTSTCKVVKTKT 540  
 QY 541 YCLSIABISNTLFGFPRIVPLVEILKNDGVREARSG 577  
 DB 541 YCLSIABISNTLFGFPRIVPLVEILKNDGVREARSG 577

RESULT 6  
 AAM06827  
 ID AAM06827 standard; Protein; 577 AA.

AC AAM06827;  
 DT 03-MAR-1997 (first entry)  
 DE Newcastle disease virus haemagglutinin.

XX Turkey herpes virus; recombinant virus; vaccine; prophylaxis;  
 KM immunisation; avian virus; infectious bronchitis virus;  
 KM infectious bursal disease virus; Newcastle disease virus;  
 KM Marek's disease virus; infectious laryngotracheitis virus; IBV;  
 KM IBV; NDV; MDV; ILV.  
 OS Newcastle disease virus.

PN MO9605291-A1.  
 PD 22-FEB-1996.

PF 09-AUG-1995; 95WO-US10245.  
 PR 22-DEC-1994; 94US-0362240.  
 PR 09-AUG-1994; 94US-0288065.

PA (SYTR ) SYNTRO CORP.

PI Cochran MD, Junker DE, Singer PA, Wild MA;  
 DR MPI, 1996-139689/14.  
 DR N-PSDB; AAT16205.

XX Recombinant turkey herpes viruses contg. foreign DNA encoding a  
 PT cytokine - useful in vaccines to protect against Marek's disease  
 PT virus and other avian viruses.

PS Disclosure: Page 175-176; 249PD; English.

XX Recombinant turkey herpes virus (rTH) which comprise a foreign DNA  
 CC sequence encoding a cytokine inserted into a XhoI site within an  
 CC EcoRI #9 genomic fragment, where the cytokine can be expressed in  
 CC host cells infected with the virus can be used in vaccines to  
 CC protect turkeys against avian viruses. The recombinant viruses can  
 CC be used for immunising birds against infectious bronchitis virus  
 CC (IBV), infectious bursal disease virus (IBDV), Marek's disease virus  
 CC (MDV) infectious laryngotracheitis virus (ILV) and Newcastle disease

CC virus (NDV). They may also be used in multivalent vaccines to  
 CC protect against two or more of these avian viruses. This sequence  
 CC is the haemagglutinin protein of the Newcastle disease virus, an  
 CC antigen which can be used in the recombinant vaccines.

Sequence 577 AA;

Query Match 97.4%; Score 2920; DB 17; Length 577;  
 Best Local Similarity 96.9%; Pred. No. 2.2e-275;  
 Matches 559; Conservative 8; Mismatches 10; Indels 0; Gaps 0;

QY 1 MDRAVSQVLENDEREAKNTWRLIFRIAILLTVTLTASVSLVSKGASTPSDLVGP 60  
 DB 1 MDRAVSQVLENDEREAKNTWRLIFRIAILLTVTLTASVSLVSKGASTPSDLVGP 60  
 QY 61 TRISRAEKTISALGSDNDVDVRIYKQVAALESPLALNTEFTTNATLSLYQINGANN 120  
 DB 61 TRISRAEKTISALGSDNDVDVRIYKQVAALESPLALNTEFTTNATLSLYQINGANN 120  
 QY 61 TRISRAEKTISALGSDNDVDVRIYKQVAALESPLALNTEFTTNATLSLYQINGANN 120  
 DB 61 TRISRAEKTISALGSDNDVDVRIYKQVAALESPLALNTEFTTNATLSLYQINGANN 120  
 QY 121 SGWGAPIHDPDPIGIGKEILVDNASDVSFPYAPQEHLPFAPPTGSGCTRIIPSPDM 180  
 DB 121 SGWGAPIHDPDPIGIGKEILVDNASDVSFPYAPQEHLPFAPPTGSGCTRIIPSPDM 180  
 QY 181 SATHYCYTHNVILSGCRDSSHSHQYALGVLRRTATGRIFFTLSRISLDDTONRKSCSV 240  
 DB 181 SATHYCYTHNVILSGCRDSSHSHQYALGVLRRTATGRIFFTLSRISLDDTONRKSCSV 240  
 QY 241 SATPLGCDMLCSKVTETEBEDYNSAVPTLMAHGLGFDGQHEKDLDTVTLLFEDVWVANYP 300  
 DB 241 SATPLGCDMLCSKVTETEBEDYNSAVPTLMAHGLGFDGQHEKDLDTVTLLFEDVWVANYP 300  
 QY 301 GVGGSFIDGRVWFVYGLKPNPSDPTVOEGKYIYKRYNDTCDEDDYOIRMAKSSYK 360  
 DB 301 GVGGSFIDGRVWFVYGLKPNPSDPTVOEGKYIYKRYNDTCDEDDYOIRMAKSSYK 360  
 QY 361 GVGGSFIDGRVWFVYGLKPNPSDPTVOEGKYIYKRYNDTCDEDDYOIRMAKSSYK 420  
 DB 361 GVGGSFIDGRVWFVYGLKPNPSDPTVOEGKYIYKRYNDTCDEDDYOIRMAKSSYK 420  
 QY 421 FSPALLYPMYVSNKTATLHSPYTFNAFTPGSIPCOASARCPNSCVTVGYTDPYPLIFR 480  
 DB 421 FSPALLYPMYVSNKTATLHSPYTFNAFTPGSIPCOASARCPNSCVTVGYTDPYPLIFR 480  
 QY 481 NHTLRGVGTMLDSEQARLNPAFAVFDSTSRITRVSSSTKAYTTSTCKVVKTKT 540  
 DB 481 NHTLRGVGTMLDSEQARLNPAFAVFDSTSRITRVSSSTKAYTTSTCKVVKTKT 540  
 QY 541 YCLSIABISNTLFGFPRIVPLVEILKNDGVREARSG 577  
 DB 541 YCLSIABISNTLFGFPRIVPLVEILKNDGVREARSG 577

RESULT 7  
 AAY51232  
 ID AAY51232 standard; Protein; 577 AA.  
 AC AAY51232;  
 DT 07-APR-2000 (first entry)  
 DE Newcastle disease virus LaSota genome encoded protein 5.  
 KM Avian-paramyxovirus; infection; lentogenic; F protein; vaccine;  
 KM respiratory disease; gastrointestinal disease; poultry pathogen;  
 KM local immunity.  
 OS Newcastle disease virus.  
 PN MO9966045-A1.  
 PD 23-DEC-1999.  
 PF 17-JUN-1999; 99WO-NL00377.

XX 19-JUN-1998; 98BP-0202054.  
XX (DIEN-) STICHTING DIENST LANDBOUWKUNDIG ONDERZOE.  
XX Peeters BPH, De Leeuw OS, Koch G, Gielkens ALJ;  
XX MPI; 2000-106102/09.  
XX New avian paramyxovirus cDNA, useful for production of vaccine against  
XX Newcastle disease virus -  
XX  
XX Disclosure; Fig 3; 115p; English.  
XX This invention describes a novel avian-paramyxovirus cDNA (I) which  
XX comprises a nucleic acid sequence corresponding to the 5' terminal  
XX end of the genome of avian-paramyxovirus allowing the generation of  
XX an infectious copy of avian-paramyxovirus. The cell line is useful for  
XX the production of infectious lentogenic NDV (Newcastle Disease virus)  
XX without the addition of exogenous proteolytic activity. Also it is  
XX possible to generate a stable transfected cell line that expresses the  
XX wild-type F protein in the virus envelope therefore providing infectious  
XX particles, useful in the form of a vaccine, especially against  
XX respiratory and/or gastrointestinal diseases. NDV can be easily cultured  
XX to very high titers in embryonated eggs. Mass culture of embryonated  
XX eggs is relatively cheap. NDV vaccines are relatively stable and can be  
XX simply administered by mass application methods e.g. drinking water or  
XX by spraying or by aerosol formation. The natural route of infection is  
XX by the respiratory and/or gastrointestinal tract which are also the major  
XX routes of infection of many other poultry pathogens. NDV can induce local  
XX immunity despite the presence of circulating maternal antibody. This  
XX sequence represents a protein encoded by the NDV strain Iasiota genome  
XX which is described in the method of the invention.

SQ Sequence 577 AA;

Query Match 97.4%; Score 2920; DB 21; Length 577;

Best Local Similarity 97.1%; Pred. No. 2.2e-275;

Matches 560; Conservative 8; Mismatches 9; Indels 0; Gaps 0;

DB 1 MDRAVSVVALENDEREAKNTWRLIFRIAILLVTLATVAVSLVSMGASTSDLVGIP 60  
QY 1 MDRAVSVVALENDEREAKNTWRLIFRIAILLVTLATVAVSLVSMGASTSDLVGIP 60  
DB 1 MDRAVSVVALENDEREAKNTWRLIFRIAILLVTLATVAVSLVSMGASTSDLVGIP 60  
QY 61 TRISRAEKTITSLAGSNQDVDRIRYKQVALESPALINTEETIMNATISYINGAANN 120  
DB 61 TRISRAEKTITSLAGSNQDVDRIRYKQVALESPALINTEETIMNATISYINGAANN 120  
QY 121 SGWGAPIHDPFIIGIGKELIVNASDVTSPYSAFOEHLNFIPTPTGSGCTTRISPFDM 180  
DB 121 SGWGAPIHDPFIIGIGKELIVNASDVTSPYSAFOEHLNFIPTPTGSGCTTRISPFDM 180  
QY 181 SATHYCTTHNVILSGCDHSHSHOYLALGVLTATRTATRTIFSTLRSLDDTONRKSQSV 240  
DB 181 SATHYCTTHNVILSGCDHSHSHOYLALGVLTATRTATRTIFSTLRSLDDTONRKSQSV 240  
QY 241 SATPLGCDMCSKTEETEEEDYNSAVPTLMAHGLIGDQGYHEKODLVTLTFEDWANYP 300  
DB 241 SATPLGCDMCSKTEETEEEDYNSAVPTLMAHGLIGDQGYHEKODLVTLTFEDWANYP 300  
QY 301 GVGGSFIDRWFVSFVYGLKPNSPDVTQEGKVITYKRNNDTCPEBODYQIIMAKSSYK 360  
DB 301 GVGGSFIDRWFVSFVYGLKPNSPDVTQEGKVITYKRNNDTCPEBODYQIIMAKSSYK 360  
QY 361 PGRFGKRIQOAILISIVSTSLGEDPVLTPVPNTVTLMAEGRIITVGTSHFLYORGSY 420  
DB 361 PGRFGKRIQOAILISIVSTSLGEDPVLTPVPNTVTLMAEGRIITVGTSHFLYORGSY 420  
QY 421 FSRPALLYPMVNSKATLHSPYTFNATRBGSI PCQASARCPNSCVGVYTDYDPLIFR 480  
DB 421 FSRPALLYPMVNSKATLHSPYTFNATRBGSI PCQASARCPNSCVGVYTDYDPLIFR 480  
QY 481 NHTLRGVFTMLDSEQARLNPASAVPDSRSTRITRVSSSSRAAYTTSTCFKVVXNTKT 540  
DB 481 NHTLRGVFTMLDSEQARLNPASAVPDSRSTRITRVSSSSRAAYTTSTCFKVVXNTKT 540

DB 481 NHTLRGVFTMLDSEQARLNPASAVPDSRSTRITRVSSSSRAAYTTSTCFKVVXNTKT 540  
QY 541 YCLISIAEISNTLFGERRIVPLLVETIKNDGVREARSG 577  
DB 541 YCLISIAEISNTLFGERRIVPLLVETIKNDGVREARSG 577

RESULT 8

AAR58859 standard; Protein; 581 AA.

AAR58859;

25-MAR-2003 (updated)

13-APR-1995 (first entry)

Newcastle Disease Virus HN gene product.

Self fragment; Newcastle Disease Virus; HN gene.

Synthetic.

MO9419014-A1.

01-SEP-1994.

28-FEB-1994; 94MO-US01826.

26-FEB-1993; 93US-0024156.

(JAPG ) NIPPON ZEON KK.

(SYTR ) SYNTRO CORP.

Cochran MD;

MPI; 1994-294007/36.

N-PSDB; AAQ68943.

New recombinant fowl pox virus for use in vaccines - contains genes expressing antigens of Newcastle disease virus and opt. infectious bronchitis virus

Disclosure; Page 68-70; 85p; English.

Newcastle Disease Virus (NDV) HN and F genes were inserted as a  
Self fragment into the homology vector 443-88.8 at the unique  
Self site. The NDV HN and F genes were inserted in the same  
transcriptional orientation as the ORF in the parental homology  
vector. The sequence of Self fragment is in AAQ68943/R58858/AAR58859.  
The inserted Self fragment has the following structure:  
CC Junction A - Fragment 1 (HN, AAs 2-577) - Junction B - Fragment  
2 (F, AAs 1-553) - Junction C - Fragment 3 (PBR322) - Junction D.  
Fragment 1 is approx. 1811 bp Avail to Neel Fragment of the NDV HN  
cDNA clone (B1 strain). Fragment 2 is an approx 1812 bp BamHI to  
PstI fragment of the full length NDV F cDNA (B1 Strain). Fragment  
3 is an approx 235 bp PstI and ScaI fragment of the plasmid PBR322.  
CC The sequences of the junctions are in AAQ68945, AAQ68946,  
CC AAQ68947 and AAQ68948.  
CC (Updated on 25-MAR-2003 to correct PN field.)

SQ Sequence 581 AA;

Query Match 97.2%; Score 2915; DB 15; Length 581;

Best Local Similarity 96.9%; Pred. No. 7e-275;

Matches 558; Conservative 8; Mismatches 10; Indels 0; Gaps 0;

QY 2 DRAVSVVALENDEREAKNTWRLIFRIAILLVTLATVAVSLVSMGASTSDLVGIP 61  
DB 6 DRAVSVVALENDEREAKNTWRLIFRIAILLVTLATVAVSLVSMGASTSDLVGIP 65  
QY 62 RISRAEKTITSLAGSNQDVDRIRYKQVALESPALINTEETIMNATISYINGAANN 121  
DB 62 RISRAEKTITSLAGSNQDVDRIRYKQVALESPALINTEETIMNATISYINGAANN 121

Db 66 RISRAEKITSTLGSNDVDRIYKQVALBESPLALNTETIMMAITSLSQINGAANS 125  
 Qy 122 GMAPIHDPDFIGIGKELIVDNASDVTSFYPSAFOEHLNFIPTTSGGCTRIIPSPDMS 181  
 Db 126 GMAPIHDPDVIIGIGKELIVDDASDVTSFYPSAFOEHLNFIPTTSGGCTRIIPSPDMS 185  
 Qy 182 ATHCYTHNVILSGCRHSHSHQYIALGVLTATGRIIPFSTLRSISLDDTQNRKSCSVS 241  
 Db 186 ATHCYTHNVILSGCRHSHSHQYIALGVLTATGRIIPFSTLRSISLDDTQNRKSCSVS 245  
 Qy 242 ATPGCDMLCSKATETEEDYNASAVPTLMAGRIAGFDQYHEKDLDTTLFEDWVANYPG 301  
 Db 246 ATPGCDMLCSKATETEEDYNASAVPTLMAGRIAGFDQYHEKDLDTTLFEDWVANYPG 305  
 Qy 302 VGGGSFIDGRWFSYVGLKPNPSDVTQEGKYVIYKRYNDTCPEODYOIRMAKSSYKP 361  
 Db 306 VGGGSFIDSRWFSYVGLKPNTPSDVTQEGKYVIYKRYNDTCPEODYOIRMAKSSYKP 365  
 Qy 362 GRFGGKRIQOAILSIKYSTLSGEDPVLTPPNTVTLMGAEGRILTVGTSHELYORGSSYF 421  
 Db 366 GRFGGKRIQOAILSIKYSTLSGEDPVLTPPNTVTLMGAEGRILTVGTSHELYORGSSYF 425  
 Qy 422 SPALLYPMTVSNKATLHSPYTFNAFTRPGSIPCOASARCPNSCVTVGYTDPYPLIFRYN 481  
 Db 426 SPALLYPMTVSNKATLHSPYTFNAFTRPGSIPCOASARCPNSCVTVGYTDPYPLIFRYN 485  
 Qy 482 HTLGVFGTMDSEQARLNPASAVFDSRSRITRVSSSTKAAYTTSTCFKVVKTNTKY 541  
 Db 486 HTLGVFGTMDSEQARLNPASAVFDSRSRITRVSSSTKAAYTTSTCFKVVKTNTKY 545  
 Qy 542 CLSTIAEISNTLFGFRIYVPLVEILKNDGVREARSG 577  
 Db 546 CLSTIAEISNTLFGFRIYVPLVEILKNDGVREARSG 581

## RESULT 9

AARS598  
 ID AARS598 standard; Protein; 581 AA.

AC AARS598;  
 XX  
 DT 25-MAR-2003 (updated)  
 DT 14-APR-1995 (first entry)  
 XX  
 DE Newcastle disease virus HN gene product.  
 XX  
 KM Newcastle disease virus; HN gene; SfiI; vector 502-26.22.  
 XX  
 OS Synthetic.  
 XX  
 FN MO9419015-A1.  
 XX  
 XX 01-SEP-1994.  
 PD  
 XX 28-FEB-1994; 94MO-US02252.  
 PF  
 XX 26-FEB-1993; 93US-0024156.  
 PR  
 XX (SYTR ) SYNTRO CORP.  
 PA  
 XX Cochran MD;  
 PI  
 XX MPI; 1994-294008/36.  
 DR N-PSDB; AA070570.  
 XX  
 XX New recombinant fowl pox viruses - useful as vaccines against  
 FT fowl pox virus, Newcastle Disease Virus and infectious  
 PT laryngotracheitis virus.  
 XX  
 PS Disclosure; Page 77-79; 97pp; English.  
 XX  
 CC AA070570 is the SfiI fragment insert in Homology Vector 502-26.22  
 CC contg. Newcastle disease virus (NDV) HN and F genes. The structure

CC of the fragment is: 5'- Junction A - Fragment 1 (NDV HN AAs 2-577)  
 CC - Junction B - Fragment 2 (NDV F AAs 1-553) - Junction C - Fragment  
 CC 3 (PB3322) - Junction D - 3'. Fragment 1 is Avail to NaeI fragment  
 CC of the full length NDV HN cDNA clone (B1 strain). Fragment 2 is  
 CC BamHI to PstI fragment of the full length NDV F cDNA (B1 strain).  
 CC Fragment 3 is a PstI and ScaI fragment of PB3322. The structures  
 CC of the Junctions A, B, C and D are given in AA070552, AA070553,  
 CC AA070554 and AA070555 respectively.  
 CC (updated on 25-MAR-2003 to correct PN field.)  
 XX

## Sequence 581 AA;

Query Match 97.2%; Score 2915; DB 15; Length 581;  
 Best Local Similarity 96.9%; Pred. No. 7e-275;  
 Matches 558; Conservative 8; Mismatches 10; Indels 0; Gaps 0;

Qy 2 DRANSQVALNDEDEAKNTWELFRIMILLITVTLATSVASLYSNGASTPSDLVGIPT 61  
 Db 6 DRAVSQVALNDEDEAKNTWELFRIMILLITVTLATSVASLYSNGASTPSDLVGIPT 65  
 Qy 62 RISRAEKITSTLGSNDVDRIYKQVALBESPLALNTETIMMAITSLSQINGAANS 121  
 Db 66 RISRAEKITSTLGSNDVDRIYKQVALBESPLALNTETIMMAITSLSQINGAANS 125  
 Qy 122 GMAPIHDPDFIGIGKELIVDNASDVTSFYPSAFOEHLNFIPTTSGGCTRIIPSPDMS 181  
 Db 126 GMAPIHDPDVIIGIGKELIVDDASDVTSFYPSAFOEHLNFIPTTSGGCTRIIPSPDMS 185  
 Qy 182 ATHCYTHNVILSGCRHSHSHQYIALGVLTATGRIIPFSTLRSISLDDTQNRKSCSVS 241  
 Db 186 ATHCYTHNVILSGCRHSHSHQYIALGVLTATGRIIPFSTLRSISLDDTQNRKSCSVS 245  
 Qy 242 ATPGCDMLCSKATETEEDYNASAVPTLMAGRIAGFDQYHEKDLDTTLFEDWVANYPG 301  
 Db 246 ATPGCDMLCSKATETEEDYNASAVPTLMAGRIAGFDQYHEKDLDTTLFEDWVANYPG 305  
 Qy 302 VGGGSFIDGRWFSYVGLKPNPSDVTQEGKYVIYKRYNDTCPEODYOIRMAKSSYKP 361  
 Db 306 VGGGSFIDSRWFSYVGLKPNTPSDVTQEGKYVIYKRYNDTCPEODYOIRMAKSSYKP 365  
 Qy 362 GRFGGKRIQOAILSIKYSTLSGEDPVLTPPNTVTLMGAEGRILTVGTSHELYORGSSYF 421  
 Db 366 GRFGGKRIQOAILSIKYSTLSGEDPVLTPPNTVTLMGAEGRILTVGTSHELYORGSSYF 425  
 Qy 422 SPALLYPMTVSNKATLHSPYTFNAFTRPGSIPCOASARCPNSCVTVGYTDPYPLIFRYN 481  
 Db 426 SPALLYPMTVSNKATLHSPYTFNAFTRPGSIPCOASARCPNSCVTVGYTDPYPLIFRYN 485  
 Qy 482 HTLGVFGTMDSEQARLNPASAVFDSRSRITRVSSSTKAAYTTSTCFKVVKTNTKY 541  
 Db 486 HTLGVFGTMDSEQARLNPASAVFDSRSRITRVSSSTKAAYTTSTCFKVVKTNTKY 545  
 Qy 542 CLSTIAEISNTLFGFRIYVPLVEILKNDGVREARSG 577  
 Db 546 CLSTIAEISNTLFGFRIYVPLVEILKNDGVREARSG 581

## RESULT 10

AAW10690  
 ID AAW10690 standard; Protein; 581 AA.

AC AAW10690;  
 XX  
 DT 05-MAY-1997 (first entry)  
 DT  
 XX  
 DE Newcastle disease virus haemagglutinin.  
 DB  
 XX Fowlpox virus; FPV; recombinant virus; vector; vaccine;  
 KM immunisation; NDV; haemagglutinin; fusion protein; antigen;  
 XX poultry.  
 XX  
 XX Newcastle disease virus.

PN MO640880-A1.  
 XX  
 PD 19-DEC-1996.  
 XX  
 PF 04-JUN-1996; 96MO-US11187.  
 XX  
 PR 07-JUN-1995; 95US-0484790.  
 XX  
 XX (SYTR ) SYNTRO CORP.  
 PI Cochran MD, Junker DE, Singer PA;  
 DR WPI; 1997-087060/08.  
 DR N-PSDB; AAT48510.  
 XX  
 PT New recombinant fowlpox virus - contg. a foreign DNA sequence  
 PT inserted into the fowlpox virus genome, used for the prodn. of  
 PT vaccines.  
 XX  
 PS Disclosure; Page 107-108; 134pp; English.  
 XX  
 CC Newcastle disease virus (NDV) haemagglutinin (HN) (AAM10690) and  
 CC fusion (F) protein (AAM10691) are expressed by novel recombinant  
 CC fowlpox virus (FPV). The genes (see also AAT48510) for HN and F can  
 CC be inserted into homology vector 443-88.8 (see also AAT48511) at the  
 CC unique SfiI site, yielding homology vector 502-26.22 (see also  
 CC AAT48502-05), which can be used to insert the NDV HN and F genes  
 CC into fowlpox virus. The recombinant virus is used to deliver the  
 CC vaccine antigens to poultry.  
 XX  
 SQ Sequence 581 AA;  
 Query Match 97.2%; Score 2915; DB 18; Length 581;  
 Best Local Similarity 96.9%; Pred. No. 7e-275;  
 Matches 558; Conservative 8; Mismatches 10; Indels 0; Gaps 0;  
 QY 2 DRAVSQVLENDEREAKNTWRLIFRIAILLTVTTLATSVASLYSMGASTPSDLVGIP 61  
 DB 6 DRAVSQVLENDEREAKNTWRLIFRIAILLTVTTLATSVASLYSMGASTPSDLVGIP 65  
 QY 62 RISRAEKKITTSALGSNODVVDRIYKQVALSPALANTETTMMNATISLYQINGAANS 121  
 DB 66 RISRAEKKITTSALGSNODVVDRIYKQVALSPALANTETTMMNATISLYQINGAANS 125  
 QY 122 GMGAPIHDPDFIGIGKELIVDNASDVTSFYPFAFOEHLNFIAPPTGSGCTRIIPFDM 181  
 DB 126 GMGAPIHDPDFIGIGKELIVDNASDVTSFYPFAFOEHLNFIAPPTGSGCTRIIPFDM 185  
 QY 182 ATHYCYTHNVILSGCRDHS HQYLALGVLTATGRIFPSTLRSLSDDTQNRKSCSV 241  
 DB 186 ATHYCYTHNVILSGCRDHS HQYLALGVLTATGRIFPSTLRSLSDDTQNRKSCSV 245  
 QY 242 ATPFGCDMLCSKVTETEEBDYNSAVPTLMAHGRIGFGQYHEKDLVTTLPFGWVANYPG 301  
 DB 246 ATPFGCDMLCSKVTETEEBDYNSAVPTLMAHGRIGFGQYHEKDLVTTLPFGWVANYPG 305  
 QY 302 VGGSSFTIDGRWFSVGGIKENPSDPTVQSGKYIYKRYNDTCDEDDYQIRMAKSSYK 361  
 DB 306 VGGSSFTIDGRWFSVGGIKENPSDPTVQSGKYIYKRYNDTCDEDDYQIRMAKSSYK 365  
 QY 362 GRFGKRIIOQAALISIKVTSLSGEDPVLTPPNTVTLGAGRILTVTSHFLYQSGSYF 421  
 DB 366 GRFGKRIIOQAALISIKVTSLSGEDPVLTPPNTVTLGAGRILTVTSHFLYQSGSYF 425  
 QY 422 SPALLYMTVSNKATLHSPYTFNAFTRPGSIPCOASARCPNSCVTVYDPPYPLIFRYN 481  
 DB 426 SPALLYMTVSNKATLHSPYTFNAFTRPGSIPCOASARCPNSCVTVYDPPYPLIFRYN 485  
 QY 482 HTLRGVTGTMLDGQALNPASAFDSTSRIRIVSSSSSTKAAVTTSTCFKVVKNKTY 541  
 DB 486 HTLRGVTGTMLDGQALNPASAFDSTSRIRIVSSSSSTKAAVTTSTCFKVVKNKTY 545  
 QY 542 CLSIAEISNTLFGFRIIVPLLVLEILKNDGVREARSG 577

DB 546 CLSIAEISNTLFGFRIIVPLLVLEILKNDGVREARSG 581  
 RESULT 11  
 AAY21982  
 ID AAY21982 standard; Protein; 581 AA.  
 XX  
 XX AAY21982;  
 AC  
 XX  
 DT 07-SEP-1999 (first entry)  
 XX  
 DE Seq ID No: 13 of US925358.  
 XX  
 KM Fowlpox virus; FPV; recombinant; vaccine; immunisation; chicken; NDV;  
 KM Newcastle disease virus; NDV; Fowlpox; Infectious Laryngotracheitis.  
 XX  
 OS Fowlpox virus.  
 XX  
 PN US925358-A.  
 XX  
 PD 20-JUL-1999.  
 XX  
 PF 07-JUN-1995; 95US-0484575.  
 XX  
 PR 07-JUN-1995; 95US-0484575.  
 PR 26-FEB-1993; 93US-0024156.  
 PR 28-FEB-1994; 94MO-US02252.  
 XX  
 PA (SYTR ) SYNTRO CORP.  
 XX  
 PI Cochran MD, Junker DE;  
 DR WPI; 1999-418249/35.  
 DR N-PSDB; AAX81147.  
 XX  
 PT Fowlpox viruses, useful as vaccines for immunization of  
 PT chickens/turkeys against Fowlpox and Newcastle disease virus  
 XX  
 PS Disclosure; Column 61-70; 108pp; English.  
 CC  
 CC The invention relates to a recombinant fowlpox virus (FPV) comprising  
 CC a foreign DNA inserted into a region of the fowlpox virus genome  
 CC corresponding to a 2.8 kb EcoRI fragment, capable of being expressed in a  
 CC host cell. The virus is used as a vaccine for immunising chickens against  
 CC Newcastle disease virus (NDV), Fowlpox, and Infectious Laryngotracheitis.  
 XX  
 SQ Sequence 581 AA;  
 Query Match 97.2%; Score 2915; DB 20; Length 581;  
 Best Local Similarity 96.9%; Pred. No. 7e-275;  
 Matches 558; Conservative 8; Mismatches 10; Indels 0; Gaps 0;  
 QY 2 DRAVSQVLENDEREAKNTWRLIFRIAILLTVTTLATSVASLYSMGASTPSDLVGIP 61  
 DB 6 DRAVSQVLENDEREAKNTWRLIFRIAILLTVTTLATSVASLYSMGASTPSDLVGIP 65  
 QY 62 RISRAEKKITTSALGSNODVVDRIYKQVALSPALANTETTMMNATISLYQINGAANS 121  
 DB 66 RISRAEKKITTSALGSNODVVDRIYKQVALSPALANTETTMMNATISLYQINGAANS 125  
 QY 122 GMGAPIHDPDFIGIGKELIVDNASDVTSFYPFAFOEHLNFIAPPTGSGCTRIIPFDM 181  
 DB 126 GMGAPIHDPDFIGIGKELIVDNASDVTSFYPFAFOEHLNFIAPPTGSGCTRIIPFDM 185  
 QY 182 ATHYCYTHNVILSGCRDHS HQYLALGVLTATGRIFPSTLRSLSDDTQNRKSCSV 241  
 DB 186 ATHYCYTHNVILSGCRDHS HQYLALGVLTATGRIFPSTLRSLSDDTQNRKSCSV 245  
 QY 242 ATPFGCDMLCSKVTETEEBDYNSAVPTLMAHGRIGFGQYHEKDLVTTLPFGWVANYPG 301  
 DB 246 ATPFGCDMLCSKVTETEEBDYNSAVPTLMAHGRIGFGQYHEKDLVTTLPFGWVANYPG 305



QY 302 VGGSGFIDGRWFSYVGGGLKENSBDTVQEGKYIYKRYNDTCPEBDYQIRMAKSSYKP 361  
DB 306 VGGGFFIDSRWFSYVGGGLKENTPBDTVQEGKYIYKRYNDTCPEBDYQIRMAKSSYKP 365  
QY 362 GRFGGKRIQOAILSTIKYSTSLGEDPVLTPPNTVTLMAEGRIITVGTSHFLYQSGSYF 421  
DB 366 GRFGGKRIQOAILSTIKYSTSLGEDPVLTPPNTVTLMAEGRIITVGTSHFLYQSGSYF 425  
QY 422 SPALLPMTVSNKATLHSPYTFNAFTRPGSIPCOASARCPNSCVTGYTDPYPLIFRYN 481  
DB 426 SPALLPMTVSNKATLHSPYTFNAFTRPGSIPCOASARCPNSCVTGYTDPYPLIFRYN 485  
QY 482 HTLRGVFGTMDSEQARLNPAASAVPDSRSRIRTVSSSSSTKAAVYTSCTCKVVKTKNTY 541  
DB 486 HTLRGVFGTMDSEQARLNPAASAVPDSRSRIRTVSSSSSTKAAVYTSCTCKVVKTKNTY 545  
QY 542 CLSTIAEISNTLFGFRIYPLVLEILKNDGVREARSG 577  
DB 546 CLSTIAEISNTLFGFRIYPLVLEILKNDGVREARSG 581

## RESULT 12

AAB36038  
ID AAB36038 standard; Protein; 581 AA.

AC AAB36038;  
DT 02-MAR-2001 (first entry)

DE Protein encoded by NDV SfiI fragment.

KW Fowlpox virus; FPV; antiviral; antibacterial; vaccine;  
KM Newcastle's disease virus; NDV; Marek's disease;  
XX infectious laryngotracheitis.

OS Newcastle's disease virus.

PN US6136318-A.

PD 24-OCT-2000.

PF 07-JUN-1995; 95US-0486414.

PR 26-FEB-1993; 93US-0024156.

PR 28-FEB-1994; 94WO-US02252.

PA (JUNK/) JUNKER D E.

PA (COCH/) COCHRAN M D.

PI Cochran MD, Junker DE;

DR MPI: 2000-686071/67.

DR N-PSDB; AAC67862.

PS New recombinant fowlpox virus useful as vaccines contains foreign DNA inserted into specific non-essential region of the genome -

XX Disclosure: Column 69-72; 56pp; English.

XX The present sequence is provided in a specification relating to a

CC recombinant fowlpox virus (FPV) that comprises a foreign DNA inserted

CC within a 3.5 kb SfiI fragment of the FPV genomic DNA. The foreign DNA

CC can be expressed in host cells infected with FPV. The recombinant FPV

CC may be used in vaccines to protect animals (especially chickens) against

CC fowlpox and, depending on the source of the foreign DNA, other diseases,

CC particularly Newcastle's disease, Marek's disease or infectious

XX laryngotracheitis.

XX SQ Sequence 581 AA;

Query Match 97.2%; Score 2915; DB 21; Length 581;  
Best Local Similarity 96.9%; Pred. No. 76-275;  
Matches 558; Conservative 8; Mismatches 10; Indels 0; Gaps 0;

QY 2 DRAVSQVLENDEREAKNTWRLIFRIALLITVTLATSVALYSMGASTPSDLVGIP 61  
DB 6 DRAVSQVLENDEREAKNTWRLIFRIALLITVTLATSVALYSMGASTPSDLVGIP 65  
QY 62 RISRAEEKITSLAGSNQDVDRIRYQVALBESPLALNTETTITMAITSLSQINGAANS 121  
DB 66 RISRAEEKITSLAGSNQDVDRIRYQVALBESPLALNTETTITMAITSLSQINGAANS 125  
QY 122 GMGAPIDHDPDIFIGIGELIYDNASDVTSPFSAFOEHLNFIAPPTSGGCTRIIPSPMS 181  
DB 126 GMGAPIDHDPDIFIGIGELIYDNASDVTSPFSAFOEHLNFIAPPTSGGCTRIIPSPMS 185  
QY 182 ATHCYTHNVILSGCRDHSRSHQYLALGVLTATGRIFFSTLRSISLDDTQNRKSCSVS 241  
DB 186 ATHCYTHNVILSGCRDHSRSHQYLALGVLTATGRIFFSTLRSISLDDTQNRKSCSVS 245  
QY 242 ATPIGCDMLCSKATETEEDYNASAVPTLMAHGRIGPDQYHEKLDVTTLFEDVANYPG 301  
DB 246 ATPIGCDMLCSKATETEEDYNASAVPTLMAHGRIGPDQYHEKLDVTTLFEDVANYPG 305  
QY 302 VGGSGFIDGRWFSYVGGGLKENSBDTVQEGKYIYKRYNDTCPEBDYQIRMAKSSYKP 361  
DB 306 VGGGFFIDSRWFSYVGGGLKENTPBDTVQEGKYIYKRYNDTCPEBDYQIRMAKSSYKP 365  
QY 362 GRFGGKRIQOAILSTIKYSTSLGEDPVLTPPNTVTLMAEGRIITVGTSHFLYQSGSYF 421  
DB 366 GRFGGKRIQOAILSTIKYSTSLGEDPVLTPPNTVTLMAEGRIITVGTSHFLYQSGSYF 425  
QY 422 SPALLPMTVSNKATLHSPYTFNAFTRPGSIPCOASARCPNSCVTGYTDPYPLIFRYN 481  
DB 426 SPALLPMTVSNKATLHSPYTFNAFTRPGSIPCOASARCPNSCVTGYTDPYPLIFRYN 485  
QY 482 HTLRGVFGTMDSEQARLNPAASAVPDSRSRIRTVSSSSSTKAAVYTSCTCKVVKTKNTY 541  
DB 486 HTLRGVFGTMDSEQARLNPAASAVPDSRSRIRTVSSSSSTKAAVYTSCTCKVVKTKNTY 545  
QY 542 CLSTIAEISNTLFGFRIYPLVLEILKNDGVREARSG 577  
DB 546 CLSTIAEISNTLFGFRIYPLVLEILKNDGVREARSG 581

## RESULT 13

AAY58182  
ID AAY58182 standard; Protein; 581 AA.

AC AAY58182;

DT 14-MAR-2000 (first entry)

DE NDV haemagglutinin-neuraminidase (HN).

KW Fowlpox virus; FPV; recombinant; antigenic protein; expression;

KM infectious laryngotracheitis virus; ILTV; Newcastle disease virus; NDV;

KW Marek's disease virus; cytokine; promoter; homologous recombination;

KX homology vector; multivalent; live vaccine; haemagglutinin;

XX neuraminidase.

OS Newcastle disease virus.

XX Key Location/Qualifiers

XX Domain 31..57

XX US6001369-A.

XX 14-DEC-1999.

XX 07-JUN-1995; 95US-0477459.

XX 26-FEB-1993; 93US-0024156.

XX 28-FEB-1994; 94WO-US02252.

/note="Transmembrane anchor domain"

PA (SYTR ) SYNTRO CORP.  
 XX  
 PI Junker DE, Cochran MD;  
 XX  
 DR WPI; 2000-071638/06.  
 DR N-PSDB; AAZ49295.  
 XX  
 PT Recombinant fowlpox virus useful as a vaccine for immunizing fowl  
 PT against Marek's disease, Newcastle disease, infectious  
 PT laryngotracheitis virus and/or fowlpox  
 PS  
 PS Claim 5; Columns 69-72; 56pp; English.  
 XX  
 CC The invention relates to a recombinant fowlpox virus (FPV)  
 CC comprising a foreign DNA inserted into a 4.2 kb EcoRI fragment  
 CC of the fowlpox virus genome. The foreign DNA is capable of being  
 CC expressed in a host cell into which the fowlpox virus has been  
 CC introduced and encodes an antigenic protein. The antigenic protein  
 CC which may be expressed includes infectious laryngotracheitis virus  
 CC (ILTIV) glycoprotein B (gB) or glycoprotein D (gD, AAY58184), Newcastle  
 CC disease virus (NDV) haemagglutinin (HN, AAY58182) or fusion (F) protein  
 CC (AAY58183) and Marek's disease virus gB or gD. The foreign DNA may  
 CC alternatively encode a cytokine such as chicken myelomonocytic growth  
 CC factor (CMGF) or chicken interferon (cIFN). The foreign DNA in the  
 CC recombinant FPV is under the control of one or more synthetic pox  
 CC promoters, enabling control of strength and timing of heterologous  
 CC gene expression. The synthetic pox virus promoters that may be used are  
 CC based on promoters of the vaccinia virus and include early promoter 1  
 CC (EP1), late promoter 1 (LP1), EP2 and LP2 (AAZ49291-249294,  
 CC respectively). The recombinant FPV is generated via homologous  
 CC recombination between FPV DNA and a homology vector containing the  
 CC foreign DNA flanked by FPV sequences. The recombinant fowlpox viruses of  
 CC the invention are used as multivalent live vaccines for immunising fowl  
 CC against Marek's disease virus, NDV, ILTV and/or fowlpox virus. The  
 CC present sequence represents NDV haemagglutinin-neuraminidase (HN).  
 XX  
 SQ Sequence 581 AA;  
 Query Match 97.2%; Score 2915; DB 21; Length 581;  
 Best Local Similarity 96.9%; Pred. No. 7e-275; Indels 0; Gaps 0;  
 Matches 558; Conservative 8; Mismatches 10;  
 QY 2 DRAVSQVLENDEREAKNTWRLIFRIALLTVVTLATSVASLVSMGASTPSDLVGIP 61  
 DB 6 DRAVSQVLENDEREAKNTWRLIFRIALLTVVTLATSVASLVSMGASTPSDLVGIP 65  
 QY 62 RISRAEKITSAAGSNODVDRIRYQVLESPLALNTETTINMAITSLSYQINGAANS 121  
 DB 66 RISRAEKITSAAGSNODVDRIRYQVLESPLALNTETTINMAITSLSYQINGAANS 125  
 QY 122 GWGAPHIHDPDFIGIGKELIVDNASDVTSFYPSPAFQEHNLNIPATPGSGCTRIIPSDMS 181  
 DB 126 GWGAPHIHDPDFIGIGKELIVDNASDVTSFYPSPAFQEHNLNIPATPGSGCTRIIPSDMS 185  
 QY 182 ATHYCYTHNVILSGCRDHSRSHQYLALGVLTATGRIFFSTLRSISLDTQNRKSCSV 241  
 DB 186 ATHYCYTHNVILSGCRDHSRSHQYLALGVLTATGRIFFSTLRSISLDTQNRKSCSV 245  
 QY 242 ATPGCDMLCSKVTETEEDYNSAVPTLMAHGRIGPGQYHEKDLDTTLPEDVMANYPG 301  
 DB 246 ATPGCDMLCSKVTETEEDYNSAVPTLMAHGRIGPGQYHEKDLDTTLPEDVMANYPG 305  
 QY 302 VGGSSFTDGVWVPVVGGLKPNSPSDVORGVYIYRYNDTCPEDEDYQIRNAKSSYKP 361  
 DB 306 VGGSSFTDGVWVPVVGGLKPNSPSDVORGVYIYRYNDTCPEDEDYQIRNAKSSYKP 365  
 QY 362 GREFGKRIQQAALISIKVSTLAGEPVLTVPPNTVTLMAAGRIITVSTSHFLVORGSSYF 421  
 DB 366 GREFGKRIQQAALISIKVSTLAGEPVLTVPPNTVTLMAAGRIITVSTSHFLVORGSSYF 425  
 QY 422 SPALLYPMVTNSKATILHSPYTNAFTPGSIPQASARCPNSCVTVGVTDPYPLIFRYN 481  
 DB 426 SPALLYPMVTNSKATILHSPYTNAFTPGSIPQASARCPNSCVTVGVTDPYPLIFRYN 485

QY 482 HTLRGVFGTMDSEQARLNPASAVFDPSTSRSRITRVSSSTKAAYTTSTCFKVKTKNTKY 541  
 DB 486 HTLRGVFGTMDSEQARLNPASAVFDPSTSRSRITRVSSSTKAAYTTSTCFKVKTKNTKY 545  
 QY 542 CUSIAEISNTLFGFEPRIVPLVLEILKNDGVREARSG 577  
 DB 546 CUSIAEISNTLFGFEPRIVPLVLEILKNDGVREARSG 581  
 RESULT 14  
 ID AAP6147  
 ID AAP6147 standard; protein; 616 AA.  
 XX  
 AC AAP6147;  
 XX  
 DT 25-MAR-2003 (updated)  
 DT 21-JAN-1991 (first entry)  
 XX  
 DE Sequence of Newcastle disease virus (NDV) - derived haemagglutinin  
 DE neuraminidase (HN).  
 XX  
 KM Fowlpox; vaccine.  
 XX  
 OS Newcastle disease virus.  
 XX  
 PN EP308220-A.  
 XX  
 PD 22-MAR-1989.  
 XX  
 PF 15-SEP-1988; 88EP-0308532.  
 XX  
 PR 16-SEP-1987; 87JP-0231653.  
 PR 16-SEP-1988; 88JP-0231898.  
 XX  
 PA (JAPG ) NIPPON ZEON KK.  
 XX  
 PI Yanagida N, Saeki S, Ogawa R, Kamogawa K, Hayaishi Y, Sawaguchi K;  
 XX  
 DR WPI; 1989-087589/12.  
 DR N-PSDB; AAN91000.  
 XX  
 PT Recombinant avipox virus used as vaccine for fowl -  
 PT having inserted cDNA for Newcastle disease derived  
 PT haemagglutinin neuraminidase  
 XX  
 PS Disclosure; Fig 4a-4e; 27pp; English.  
 XX  
 CC cDNA coding for NDV-derived HN prepared using D-26 strain includes two  
 CC kinds, one of which is composed of 1746 bp from 112th to 1857th and  
 CC another is composed of 1848 bp from 112th to 1959th.  
 CC (Updated on 25-MAR-2003 to correct PR field.)  
 CC (Updated on 25-MAR-2003 to correct PI field.)  
 XX  
 SQ Sequence 616 AA;  
 Query Match 95.0%; Score 2847; DB 10; Length 616;  
 Best Local Similarity 94.1%; Pred. No. 3.3e-268; Indels 0; Gaps 0;  
 Matches 543; Conservative 14; Mismatches 20;  
 QY 1 MDRAVSQVLENDEREAKNTWRLIFRIALLTVVTLATSVASLVSMGASTPSDLVGIP 60  
 DB 1 MDRAVSQVLENDEREAKNTWRLIFRIALLTVVTLATSVASLVSMGASTPSDLVGIP 60  
 QY 61 TRISRAEKITSAAGSNODVDRIRYQVLESPLALNTETTINMAITSLSYQINGAANS 120  
 DB 61 TRISRAEKITSAAGSNODVDRIRYQVLESPLALNTETTINMAITSLSYQINGAANS 120  
 QY 121 SCMGAPHIHDPDFIGIGKELIVDNASDVTSFYPSPAFQEHNLNIPATPGSGCTRIIPSDM 180  
 DB 121 SCMGAPHIHDPDFIGIGKELIVDNASDVTSFYPSPAFQEHNLNIPATPGSGCTRIIPSDM 180  
 QY 181 SATHYCYTHNVILSGCRDHSRSHQYLALGVLTATGRIFFSTLRSISLDTQNRKSCSV 240

Db 181 SATHCYTHNVLLSGCRDHS HQYLALGVLTATSGRIFFSTLRSINLDDTQNRKSCSV 240  
QY 241 SATPLGCDMLCSKYETEEDYNASAVPTLMAHGRGLGPDQYHEKDLDTTLFEDWVANYP 300  
Db 241 SATPLGCDMLCSKYETEEDYNASAIPTSMVHGRLGPDQYHEKDLDTTLFEDWVANYP 300  
QY 301 GVGGSFIDGRVWFVSYGGLKPNSPSDTVQEGKYVIYKRYNDTCPEDDYQIRMAKSSYK 360  
Db 301 GVGGSFIDNRVWFVSYGGLKPNSPSDTVQEGKYVIYKRYNDTCPEDDYQIRMAKSSYK 360  
QY 361 PGRFGKRIQOAILISIKVSTSLGSDPVLTVPNTVTLGAGRGVLTGTSHPFYQSGSSY 420  
Db 361 PGRFGKRIQOAILISIKVSTSLGSDPVLTVPNTVTLGAGRGVLTGTSHPFYQSGSSY 420  
QY 421 FSPALLYPMYVSNKATLHSPYTFNAFTRPQGISIPCOASARCPNSCVTVYDPPYLFYR 480  
Db 421 FSPALLYPMYVSNKATLHSPYTFNAFTRPQGISIPCOASARCPNSCVTVYDPPYLFYR 480  
QY 481 NHTLRGVGTMLDSEQARLNPASAVFDSISRIRTRVSSSTKAAVTTSTCFKVVKTNTK 540  
Db 481 NHTLRGVGTMLDSEQARLNPASAVFDSISRIRTRVSSSTKAAVTTSTCFKVVKTNTK 540  
QY 541 YCLSTIAEISNTLFGFRIYVPLVLEILKDDGVREARSG 577  
Db 541 YCLSTIAEISNTLFGFRIYVPLVLEILKDDGVREARSG 577

## RESULT 15

AAR06329 standard; protein; 616 AA.

AAR06329;

18-DEC-1990 (first entry)

Newcastle disease virus haemagglutinin neuraminidase gene product.

Fowl pox virus; Newcastle disease antigen; vaccine;

haemagglutinin neuraminidase;

Newcastle disease virus.

W03007581-A.

12-JUL-1990.

28-DEC-1989; 89WO-J001330.

28-MAR-1989; 89JP-0076025.

29-DEC-1988; 88JP-0335605.

(JAFG ) NIPPON ZEON KK.

Ogawa R, Yanagida N, Saeki S, Ohkawa S;

MPI; 1990-239051/31.

N-PSDB; AA005549.

Promoter DNA derived from avipox virus, and chimera gene - can be

used to produce recombinant avipox virus for vaccine manufacture

Disclosure; Page ?; ?pp; Japanese.

Promoter fragment may be attached to a viral antigen, such as a

Newcastle disease antigen eg Haemagglutinin neuraminidase. This may

be expressed in a transformed host, to give a stabilised vaccine on

a large scale.

See also AA005544-8.

Sequence 616 AA;

SQ

Best Local Similarity 93.8%; Pred. No. 2e-267;  
Matches 541; Conservative 16; Mismatches 20; Indels 0; Gaps 0;

QY 1 MDRVSOVALNDRREANRRLFRITALLTVVTLATSVASIVYSGASTPDDIVCP 60  
Db 1 MDRVSOVALNDRREANRRLFRITALLTVVTLATSVASIVYSGASTPDDIVCP 60  
QY 61 TRISAEKRTSALGSNDVDRIYKOVALESPLALNTETINMATSLSYQINGAAN 120  
Db 61 TRISAEKRTSALGSNDVDRIYKOVALESPLALNTETINMATSLSYQINGAAN 120  
QY 121 SCGAPLHDPDFIGIGIKELIVNASDVTSFYPAPFQHLNFIAPPTGSGCTRIPSFDM 180  
Db 121 SCGAPLHDPDFIGIGIKELIVNASDVTSFYPAPFQHLNFIAPPTGSGCTRIPSFDM 180  
QY 181 SATHCYTHNVLLSGCRDHS HQYLALGVLTATSGRIFFSTLRSISLDDTQNRKSCSV 240  
Db 181 SATHCYTHNVLLSGCRDHS HQYLALGVLTATSGRIFFSTLRSISLDDTQNRKSCSV 240  
QY 241 SATPLGCDMLCSKYETEEDYNASAVPTLMAHGRGLGPDQYHEKDLDTTLFEDWVANYP 300  
Db 241 SATPLGCDMLCSKYETEEDYNASAIPTSMVHGRLGPDQYHEKDLDTTLFEDWVANYP 300  
QY 301 GVGGSFIDGRVWFVSYGGLKPNSPSDTVQEGKYVIYKRYNDTCPEDDYQIRMAKSSYK 360  
Db 301 GVGGSFIDNRVWFVSYGGLKPNSPSDTVQEGKYVIYKRYNDTCPEDDYQIRMAKSSYK 360  
QY 361 PGRFGKRIQOAILISIKVSTSLGSDPVLTVPNTVTLGAGRGVLTGTSHPFYQSGSSY 420  
Db 361 PGRFGKRIQOAILISIKVSTSLGSDPVLTVPNTVTLGAGRGVLTGTSHPFYQSGSSY 420  
QY 421 FSPALLYPMYVSNKATLHSPYTFNAFTRPQGISIPCOASARCPNSCVTVYDPPYLFYR 480  
Db 421 FSPALLYPMYVSNKATLHSPYTFNAFTRPQGISIPCOASARCPNSCVTVYDPPYLFYR 480  
QY 481 NHTLRGVGTMLDSEQARLNPASAVFDSISRIRTRVSSSTKAAVTTSTCFKVVKTNTK 540  
Db 481 NHTLRGVGTMLDSEQARLNPASAVFDSISRIRTRVSSSTKAAVTTSTCFKVVKTNTK 540  
QY 541 YCLSTIAEISNTLFGFRIYVPLVLEILKDDGVREARSG 577  
Db 541 YCLSTIAEISNTLFGFRIYVPLVLEILKDDGVREARSG 577

Search completed: January 2, 2004, 16:18:24  
Job time : 59 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 2, 2004, 16:16:52 ; Search time 28 Seconds

(without alignment)  
1981.762 Million cell updates/sec

Title: US-09-915-515A-1

Perfect score: 2998

Sequence: 1 MDRVSGVALBNDEKAKNT.....IVPLVEIKNDGVEARSG 577

Scoring table: BLOSUM62

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR\_76:\*

1: p1r1:\*

2: p1r2:\*

3: p1r3:\*

4: p1r4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2989	99.7	577	1 F46328	hemagglutinin-neur
2	2945	98.2	577	1 D46328	hemagglutinin-neur
3	2920	97.4	577	1 D46328	hemagglutinin-neur
4	2914	97.2	577	1 HNNZNC	hemagglutinin-neur
5	2913	97.2	577	1 HNNZNC	hemagglutinin-neur
6	2871	95.8	616	1 A46328	hemagglutinin-neur
7	2862	95.5	616	1 HNNZU1	hemagglutinin-neur
8	2849	95.0	616	1 C46328	hemagglutinin-neur
9	2848	95.0	616	1 B46328	hemagglutinin-neur
10	2846	94.9	616	1 HNNZOD	hemagglutinin-neur
11	2763	92.2	571	1 A36829	hemagglutinin-neur
12	2759	92.0	571	1 I46328	hemagglutinin-neur
13	2758	92.0	571	1 B36829	hemagglutinin-neur
14	2751	91.8	571	1 H46328	hemagglutinin-neur
15	2746	91.6	571	2 S40164	hemagglutinin-neur
16	2738.5	91.3	570	1 HNNZAV	hemagglutinin-neur
17	2719.5	90.7	581	2 S45114	hemagglutinin-neur
18	2711	90.4	571	1 C36829	hemagglutinin-neur
19	2666	88.9	571	1 D36829	hemagglutinin-neur
20	842	28.1	576	2 B37481	HN protein - Murray
21	838	28.0	568	1 HNNZ41	hemagglutinin-neur
22	781	26.1	582	1 HNNZM4	hemagglutinin-neur
23	778	26.0	571	1 HNNZP2	hemagglutinin-neur
24	777	25.9	571	1 HNNZT2	hemagglutinin-neur
25	772	25.8	565	1 HNNZC3	hemagglutinin-neur
26	771	25.7	565	1 HNNZSV	hemagglutinin-neur
27	770	25.7	582	1 HNNZMP	hemagglutinin-neur
28	766	25.6	582	1 HNNZSB	hemagglutinin-neur
29	765	25.5	565	1 HNNZC1	hemagglutinin-neur

30	765	25.5	565	1 HNNZC2	hemagglutinin-neur
31	729	24.3	576	2 A45536	hemagglutinin-neur
32	689	23.0	573	1 HNNZ4A	hemagglutinin-neur
33	480	16.0	575	1 HNNZS2	hemagglutinin-neur
34	479	16.0	575	1 HNNZSH	hemagglutinin-neur
35	479	16.0	575	2 S14532	hemagglutinin-neur
36	467	15.6	575	2 S12335	hemagglutinin-neur
37	455.5	15.2	572	1 HNNZ73	hemagglutinin-neur
38	448.5	15.0	576	1 HNNZS	hemagglutinin-neur
39	445.5	14.9	572	1 HNNZ82	hemagglutinin-neur
40	444.5	14.8	572	1 HNNZ80	hemagglutinin-neur
41	444	14.8	572	1 HNNZP3	hemagglutinin-neur
42	442.5	14.8	572	2 S37253	hemagglutinin-neur
43	441.5	14.7	572	1 HNNZB3	hemagglutinin-neur
44	441.5	14.7	572	1 HNNZ79	hemagglutinin-neur
45	441.5	14.7	575	2 A43487	hemagglutinin-neur

ALIGNMENTS

RESULT 1	F46328	hemagglutinin-neuraminidase (EC 3.2.1.-) (version 1) - Newcastle disease virus
C/Species:	Newcastle disease virus	
C/Date:	31-Dec-1993	#sequence_revision 31-Dec-1993 #text_change 18-Jun-1999
C/Accession:	F46328; A27005	
R/Sakaguchi, T.; Toyoda, T.; Gotoh, B.; Innocentio, N.M.; Kuma, K.; Miyata, T.; Nagai, Y.		
Virology 169, 260-272, 1989		
A/Title:	Newcastle disease virus evolution. I. Multiple lineages defined by sequence vari	
A/Reference number:	A46328; MUID:89204897; PMID:2705297	
A/Accession:	F46328	
A/Molecule type:	mRNA	
A/Residues:	1-577 <SAK>	
A/Cross-References:	GB:M24710, NID:g332339, PIDN:AAA46660.1, PID:g332340	
A/Experimental source:	strain BEA/45	
R/Millar, N.S.; Chamber, P.; Emerson, P.T.		
J. Gen. Virol. 67, 1917-1927, 1986		
A/Title:	Nucleotide sequence analysis of the hemagglutinin-neuraminidase gene of Newcast	
A/Reference number:	A27005; MUID:8630666; PMID:3018130	
A/Accession:	A27005	
A/Molecule type:	mRNA	
A/Residues:	1-577 <MTL>	
A/Cross-References:	GB:X04355; GB:X03634; NID:g60935; PIDN:CAA27880.1; PID:g60936	
C/Genetics:		
A/Gene:	HN	
C/Superfamily:	paramyxovirus hemagglutinin-neuraminidase	
C/Keywords:	glycoprotein; glycosidase; hemagglutinin; hydrolase; transmembrane protein	
F:2748/Domain:	transmembrane #status predicted <TMN>	
F:119,341,433,481,538/Binding site:	carbohydrate (Asn) (covalent) #status predicted	
Query Match	99.7%; Score 2989; DB 1; Length 577;	
Best Local Similarity	99.7%; Pred. No. 4.2e-222;	
Matches	575; Conservative 1; Mismatches 1; Indels 0; Gaps 0;	
Qy	1	MDRVSGVALBNDEKAKNTWRLIFRAILLTVLTATVAVSYVSGASTPBDLVGP 60
Db	1	MDRVSGVALBNDEKAKNTWRLIFRAILLTVLTATVAVSYVSGASTPBDLVGP 60
Qy	61	TRISRAEKITSAAGSNQDVDRIRYKQVALSPALANTETIMNATTSYQINGAAN 120
Db	61	TRISRAEKITSAAGSNQDVDRIRYKQVALSPALANTETIMNATTSYQINGAAN 120
Qy	121	SGWGAPIHDDPFGIGIGIKELIVDNASVYTFYPSAFQEHNFIPAPPTGGCCTRIPEFDM 180
Db	121	SGWGAPIHDDPFGIGIGIKELIVDNASVYTFYPSAFQEHNFIPAPPTGGCCTRIPEFDM 180
Qy	181	SATHYCYTHNVIIISGCRDHSCHOYLALGVLRATATGRIFPSTLRSTSLDTONRKSCSV 240
Db	181	SATHYCYTHNVIIISGCRDHSCHOYLALGVLRATATGRIFPSTLRSTSLDTONRKSCSV 240
Qy	241	SATPLGCDMLCKVTEEBEDYNSAVPTLMAHGRIGFDGYHEKDLVTTLFEDWVANYP 300
Db	241	SATPLGCDMLCKVTEEBEDYNSAVPTLMAHGRIGFDGYHEKDLVTTLFEDWVANYP 300

Db 241 SATPLGCDMLCSKVETEEDEDYNSAVPTLMAHGRGFDQYHEKDLDTTLFEDWVANYP 300  
QY 301 GVGGGSPFIDGRWVFSVYGGKPKNSPSDTVOEGKYVIYKRYNDTCPEBODYQIRMAKSSYK 360  
Db 301 GVGGGSPFIDGRWVFSVYGGKPKNSPSDTVOEGKYVIYKRYNDTCPEBODYQIRMAKSSYK 360  
QY 361 PGRFGGKRIQOAILSTIKVSTSLGSDPVLTPPNTVTLMGAEGRIILTVGSHFLYQRGSSY 420  
Db 361 PGRFGGKRIQOAILSTIKVSTSLGSDPVLTPPNTVTLMGAEGRIILTVGSHFLYQRGSSY 420  
QY 421 FSPALLPYMTVSNKATLHSPYTFNAFTRPGSIPCOASARCPNSCVTYGTYDPPYLIFFYR 480  
Db 421 FSPALLPYMTVSNKATLHSPYTFNAFTRPGSIPCOASARCPNSCVTYGTYDPPYLIFFYR 480  
QY 481 NHTLRGVFGTMDSEQARLNPAFAVFDTSRSRITRVSSSTKAAVYTTSCFKVYKTKNT 540  
Db 481 NHTLRGVFGTMDSEQARLNPAFAVFDTSRSRITRVSSSTKAAVYTTSCFKVYKTKNT 540  
QY 541 YCLSTAEISNTLFGEPRIPLVEILKNDGVREARSG 577  
Db 541 YCLSTAEISNTLFGEPRIPLVEILKNDGVREARSG 577

## RESULT 2

G46328  
hemagglutinin-neuraminidase (EC 3.2.1.-) - Newcastle disease virus  
C/Species: Newcastle disease virus  
C/Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 15-Oct-1996  
C/Acession: G46328; A29201  
R/Sakaguchi, T.; Toyoda, T.; Gotoh, B.; Innocencio, N.M.; Kuma, K.; Miyata, T.; Nagai, Y.  
Virology 169, 260-272, 1989  
A/Title: Newcastle disease virus evolution. I. Multiple lineages defined by sequence vari  
A/Reference number: A46328; MUID:89204897; PMID:2705297  
A/Acession: G46328  
A/Molecule type: mRNA  
A/Residues: 1-577 <SAK>  
A/Cross-references: GB:M24711  
R/Schaper, U.M.; Fuller, F.J.; Ward, M.D.W.; Mehrotra, Y.; Stone, H.O.; Stripp, B.R.; De  
Virology 165, 291-295, 1988  
A/Title: Nucleotide sequence of the envelope protein genes of a highly virulent, neuroto  
A/Reference number: A94379; MUID:88265873; PMID:3388773  
A/Acession: A29201  
A/Molecule type: mRNA  
A/Residues: 1-577 <SCH>  
A/Experimental source: strain Texas G.B.  
C/Genetics:  
A/Gene: HN  
C/Superfamily: paramyxovirus hemagglutinin-neuraminidase  
C/Keywords: glycoprotein; glycosidase; hemagglutinin; hydrolase; transmembrane protein  
F:27-48/Domain: transmembrane #status predicted <TMN>  
F:119,341,433,481,538/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 98.2%; Score 2945; DB 1; Length 577;

Best Local Similarity 98.1%; Pred. No. 1e-218;

Matches 566; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 1 MDRVSVQVLENDERAKNTWRLIFRIATLLTVTLATSVASLVYSGASTPSDLVGIP 60  
Db 1 MDRVSVQVLENDERAKNTWRLIFRIATLLTVTLATSVASLVYSGASTPSDLVGIP 60  
QY 61 TRISRAEKITSLAGNQVDVRIYQVALLESPLALNTETIMNATISLQINGAANN 120  
Db 61 TRISRAEKITSLAGNQVDVRIYQVALLESPLALNTETIMNATISLQINGAANN 120  
QY 121 SGWGAPIHDPDFIGIGIKELIVDNASDVTSFYPSAFOEHLNFIPTTSGGCTRIIPFDM 180  
Db 121 SGWGAPIHDPDFIGIGIKELIVDNASDVTSFYPSAFOEHLNFIPTTSGGCTRIIPFDM 180  
QY 181 SATHYCYTHNVILSGGRDHSYHOYALGVLTATATGRIFPSTIRSLSDDTQNRKSCSV 240  
Db 181 SATHYCYTHNVILSGGRDHSYHOYALGVLTATATGRIFPSTIRSLSDDTQNRKSCSV 240

QY 241 SATPLGCDMLCSKVETEEDEDYNSAVPTLMAHGRGFDQYHEKDLDTTLFEDWVANYP 300  
Db 241 SATPLGCDMLCSKVETEEDEDYNSAVPTLMAHGRGFDQYHEKDLDTTLFEDWVANYP 300  
QY 301 GVGGGSPFIDGRWVFSVYGGKPKNSPSDTVOEGKYVIYKRYNDTCPEBODYQIRMAKSSYK 360  
Db 301 GVGGGSPFIDGRWVFSVYGGKPKNSPSDTVOEGKYVIYKRYNDTCPEBODYQIRMAKSSYK 360  
QY 361 PGRFGGKRIQOAILSTIKVSTSLGSDPVLTPPNTVTLMGAEGRIILTVGSHFLYQRGSSY 420  
Db 361 PGRFGGKRIQOAILSTIKVSTSLGSDPVLTPPNTVTLMGAEGRIILTVGSHFLYQRGSSY 420  
QY 421 FSPALLPYMTVSNKATLHSPYTFNAFTRPGSIPCOASARCPNSCVTYGTYDPPYLIFFYR 480  
Db 421 FSPALLPYMTVSNKATLHSPYTFNAFTRPGSIPCOASARCPNSCVTYGTYDPPYLIFFYR 480  
QY 481 NHTLRGVFGTMDSEQARLNPAFAVFDTSRSRITRVSSSTKAAVYTTSCFKVYKTKNT 540  
Db 481 NHTLRGVFGTMDSEQARLNPAFAVFDTSRSRITRVSSSTKAAVYTTSCFKVYKTKNT 540  
QY 541 YCLSTAEISNTLFGEPRIPLVEILKNDGVREARSG 577  
Db 541 YCLSTAEISNTLFGEPRIPLVEILKNDGVREARSG 577

## RESULT 3

D46328  
hemagglutinin-neuraminidase (EC 3.2.1.-) - Newcastle disease virus (strain BI/47)  
C/Species: Newcastle disease virus  
C/Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 15-Oct-1996  
C/Acession: D46328  
R/Sakaguchi, T.; Toyoda, T.; Gotoh, B.; Innocencio, N.M.; Kuma, K.; Miyata, T.; Nagai, Y.  
Virology 169, 260-272, 1989  
A/Title: Newcastle disease virus evolution. I. Multiple lineages defined by sequence vari  
A/Reference number: A46328; MUID:89204897; PMID:2705297  
A/Acession: D46328  
A/Molecule type: mRNA  
A/Residues: 1-577 <SAK>  
A/Cross-references: GB:M24708  
C/Genetics:  
A/Gene: HN  
C/Superfamily: paramyxovirus hemagglutinin-neuraminidase  
C/Keywords: glycoprotein; glycosidase; hemagglutinin; hydrolase; transmembrane protein  
F:27-48/Domain: transmembrane #status predicted <TMN>  
F:119,341,433,481,538/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 97.4%; Score 2920; DB 1; Length 577;

Best Local Similarity 96.9%; Pred. No. 8.7e-217;

Matches 559; Conservative 8; Mismatches 10; Indels 0; Gaps 0;

QY 1 MDRVSVQVLENDERAKNTWRLIFRIATLLTVTLATSVASLVYSGASTPSDLVGIP 60  
Db 1 MDRVSVQVLENDERAKNTWRLIFRIATLLTVTLATSVASLVYSGASTPSDLVGIP 60  
QY 61 TRISRAEKITSLAGNQVDVRIYQVALLESPLALNTETIMNATISLQINGAANN 120  
Db 61 TRISRAEKITSLAGNQVDVRIYQVALLESPLALNTETIMNATISLQINGAANN 120  
QY 121 SGWGAPIHDPDFIGIGIKELIVDNASDVTSFYPSAFOEHLNFIPTTSGGCTRIIPFDM 180  
Db 121 SGWGAPIHDPDFIGIGIKELIVDNASDVTSFYPSAFOEHLNFIPTTSGGCTRIIPFDM 180  
QY 181 SATHYCYTHNVILSGGRDHSYHOYALGVLTATATGRIFPSTIRSLSDDTQNRKSCSV 240  
Db 181 SATHYCYTHNVILSGGRDHSYHOYALGVLTATATGRIFPSTIRSLSDDTQNRKSCSV 240  
QY 241 SATPLGCDMLCSKVETEEDEDYNSAVPTLMAHGRGFDQYHEKDLDTTLFEDWVANYP 300  
Db 241 SATPLGCDMLCSKVETEEDEDYNSAVPTLMAHGRGFDQYHEKDLDTTLFEDWVANYP 300  
QY 301 GVGGGSPFIDGRWVFSVYGGKPKNSPSDTVOEGKYVIYKRYNDTCPEBODYQIRMAKSSYK 360  
Db 301 GVGGGSPFIDGRWVFSVYGGKPKNSPSDTVOEGKYVIYKRYNDTCPEBODYQIRMAKSSYK 360

QY 361 PGRFGKRIQOAILISIKVSTSLGEDPVLTVPPNTVTLTGAGRILITVGTSHFLYORGSSY 420  
DB 361 PGRFGKRIQOAILISIKVSTSLGEDPVLTVPPNTVTLTGAGRILITVGTSHFLYORGSSY 420  
QY 421 FSPALLYPMVTSNKTATLHSPYTNAPTRPGSIPCOASARCPNSCVTVYTDYPLIFYYR 480  
DB 421 FSPALLYPMVTSNKTATLHSPYTNAPTRPGSIPCOASARCPNSCVTVYTDYPLIFYYR 480  
QY 481 NHTLRGVFGTMDSEORLNPASAVFDSSTSRIRTRVSSSTKAYTSTCFKVKTKNT 540  
DB 481 NHTLRGVFGTMDSEORLNPASAVFDSSTSRIRTRVSSSTKAYTSTCFKVKTKNT 540  
QY 541 YCLSIABISNTLFGFPRIVPLVLEILKNDGVREARSG 577  
DB 541 YCLSIABISNTLFGFPRIVPLVLEILKNDGVREARSG 577

## RESULT 4

hemagglutinin-neuraminidase (EC 3.2.1.-) (version 2) - Newcastle disease virus  
C/Species: Newcastle disease virus  
C/Date: 31-Mar-1988 #sequence\_revision 31-Mar-1988 #text\_change 18-Jun-1999  
C/Accession: A26355  
R/Jorgensen, E.D.; Collins, P.L.; Lomedico, P.T.  
Virology 156, 12-24, 1987  
A/Title: Cloning and nucleotide sequence of Newcastle disease virus hemagglutinin-neuraminidase  
A/Reference number: A26355; MUID:87122141; PMID:3027962  
A/Accession: A26355  
A/Molecule type: mRNA  
A/Residues: 1-577 <J0R>  
A/Cross-references: GB:M16573; NID:G332355; PID:AAA46668.1; PID:G332356  
C/Genetics:  
A/Gene: HN  
C/Superfamily: paramyxovirus hemagglutinin-neuraminidase  
C/Keywords: glycoprotein; glycosidase; hemagglutinin; hydrolase; transmembrane protein  
F:27-50/Domain: transmembrane #status predicted <TM>  
F:119,341,433,481,538/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 97.2%; Score 2914; DB 1; Length 577;  
Best Local Similarity 96.7%; Pred. No. 2.5e-216;

Matches 558; Conservative 8; Mismatches 11; Indels 0; Gaps 0;

QY 1 MDRASQVLENDREAKNTWRLIFRIALLTVVTLATSVASLVYSGASTPDLVIGIP 60  
DB 1 MDRASQVLENDREAKNTWRLIFRIALLTVVTLATSVASLVYSGASTPDLVIGIP 60  
QY 61 TRISRAEKITSAIGSNODVVDRIYKOVALESPALLNTETTINMAITSLSYQINGAANN 120  
DB 61 TRISRAEKITSAIGSNODVVDRIYKOVALESPALLNTETTINMAITSLSYQINGAANN 120  
QY 121 SGKAPLHDPDFIGIGELIVDNASDVTSPYPSAFQEHNLFIAPPTGSGCTRIIPSPDM 180  
DB 121 SGKAPLHDPDFIGIGELIVDNASDVTSPYPSAFQEHNLFIAPPTGSGCTRIIPSPDM 180  
QY 181 SATHYCYTHNVILSGCRDHSYQYLAGVLTATGRIFFSTLRSISLDDTONRKSCSV 240  
DB 181 SATHYCYTHNVILSGCRDHSYQYLAGVLTATGRIFFSTLRSISLDDTONRKSCSV 240  
QY 241 SATPLGCDMLCSKVTETEEEDYNSAVPTLMAHGLGPDQYHEKOLDVTTLFEDWVANYP 300  
DB 241 SATPLGCDMLCSKVTETEEEDYNSAVPTLMAHGLGPDQYHEKOLDVTTLFEDWVANYP 300  
QY 301 GVGGSFIDGKRWMSVYGLKPNPSPTVOEGKVIYKRYNDTPDEDDYQIRAKSSYK 360  
DB 301 GVGGSFIDGKRWMSVYGLKPNPSPTVOEGKVIYKRYNDTPDEDDYQIRAKSSYK 360  
QY 361 PGRFGKRIQOAILISIKVSTSLGEDPVLTVPPNTVTLTGAGRILITVGTSHFLYORGSSY 420  
DB 361 PGRFGKRIQOAILISIKVSTSLGEDPVLTVPPNTVTLTGAGRILITVGTSHFLYORGSSY 420  
QY 421 FSPALLYPMVTSNKTATLHSPYTNAPTRPGSIPCOASARCPNSCVTVYTDYPLIFYYR 480  
DB 421 FSPALLYPMVTSNKTATLHSPYTNAPTRPGSIPCOASARCPNSCVTVYTDYPLIFYYR 480

DB 421 FSPALLYPMVTSNKTATLHSPYTNAPTRPGSIPCOASARCPNSCVTVYTDYPLIFYYR 480  
QY 481 NHTLRGVFGTMDSEORLNPASAVFDSSTSRIRTRVSSSTKAYTSTCFKVKTKNT 540  
DB 481 NHTLRGVFGTMDSEORLNPASAVFDSSTSRIRTRVSSSTKAYTSTCFKVKTKNT 540  
QY 541 YCLSIABISNTLFGFPRIVPLVLEILKNDGVREARSG 577  
DB 541 YCLSIABISNTLFGFPRIVPLVLEILKNDGVREARSG 577

## RESULT 5

hemagglutinin-neuraminidase (EC 3.2.1.-) - Newcastle disease virus (strain IAS/46)  
C/Species: Newcastle disease virus  
C/Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 15-Oct-1996  
C/Accession: E46328  
R/Sakaguchi, T.; Toyoda, T.; Gotoh, B.; Innocencio, N.M.; Kuma, K.; Miyata, T.; Nagai, Y.  
Virology 169, 260-272, 1989  
A/Title: Newcastle disease virus evolution. I. Multiple lineages defined by sequence vari  
A/Reference number: A46328; MUID:89204897; PMID:2705297  
A/Accession: E46328  
A/Molecule type: mRNA  
A/Residues: 1-577 <SAK>  
A/Cross-references: GB:M24709  
C/Genetics:  
A/Gene: HN  
C/Superfamily: paramyxovirus hemagglutinin-neuraminidase  
C/Keywords: glycoprotein; glycosidase; hemagglutinin; hydrolase; transmembrane protein  
F:27-48/Domain: transmembrane #status predicted <TM>  
F:119,341,433,481,538/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 97.2%; Score 2913; DB 1; Length 577;  
Best Local Similarity 96.9%; Pred. No. 3e-216;

Matches 559; Conservative 8; Mismatches 10; Indels 0; Gaps 0;

QY 1 MDRASQVLENDREAKNTWRLIFRIALLTVVTLATSVASLVYSGASTPDLVIGIP 60  
DB 1 MDRASQVLENDREAKNTWRLIFRIALLTVVTLATSVASLVYSGASTPDLVIGIP 60  
QY 61 TRISRAEKITSAIGSNODVVDRIYKOVALESPALLNTETTINMAITSLSYQINGAANN 120  
DB 61 TRISRAEKITSAIGSNODVVDRIYKOVALESPALLNTETTINMAITSLSYQINGAANN 120  
QY 121 SGKAPLHDPDFIGIGELIVDNASDVTSPYPSAFQEHNLFIAPPTGSGCTRIIPSPDM 180  
DB 121 SGKAPLHDPDFIGIGELIVDNASDVTSPYPSAFQEHNLFIAPPTGSGCTRIIPSPDM 180  
QY 181 SATHYCYTHNVILSGCRDHSYQYLAGVLTATGRIFFSTLRSISLDDTONRKSCSV 240  
DB 181 SATHYCYTHNVILSGCRDHSYQYLAGVLTATGRIFFSTLRSISLDDTONRKSCSV 240  
QY 241 SATPLGCDMLCSKVTETEEEDYNSAVPTLMAHGLGPDQYHEKOLDVTTLFEDWVANYP 300  
DB 241 SATPLGCDMLCSKVTETEEEDYNSAVPTLMAHGLGPDQYHEKOLDVTTLFEDWVANYP 300  
QY 301 GVGGSFIDGKRWMSVYGLKPNPSPTVOEGKVIYKRYNDTPDEDDYQIRAKSSYK 360  
DB 301 GVGGSFIDGKRWMSVYGLKPNPSPTVOEGKVIYKRYNDTPDEDDYQIRAKSSYK 360  
QY 361 PGRFGKRIQOAILISIKVSTSLGEDPVLTVPPNTVTLTGAGRILITVGTSHFLYORGSSY 420  
DB 361 PGRFGKRIQOAILISIKVSTSLGEDPVLTVPPNTVTLTGAGRILITVGTSHFLYORGSSY 420  
QY 421 FSPALLYPMVTSNKTATLHSPYTNAPTRPGSIPCOASARCPNSCVTVYTDYPLIFYYR 480  
DB 421 FSPALLYPMVTSNKTATLHSPYTNAPTRPGSIPCOASARCPNSCVTVYTDYPLIFYYR 480  
QY 481 NHTLRGVFGTMDSEORLNPASAVFDSSTSRIRTRVSSSTKAYTSTCFKVKTKNT 540  
DB 481 NHTLRGVFGTMDSEORLNPASAVFDSSTSRIRTRVSSSTKAYTSTCFKVKTKNT 540  
QY 541 YCLSIABISNTLFGFPRIVPLVLEILKNDGVREARSG 577  
DB 541 YCLSIABISNTLFGFPRIVPLVLEILKNDGVREARSG 577

Db YCISIAEISNTLFGFRIYVLLVEILKDDGVREARSG 577

## RESULT 6

A46328 hemagglutinin-neuraminidase (EC 3.2.1.-) - Newcastle disease virus (strain D26/76)

C/Species: Newcastle disease virus

C/Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 18-Jun-1999

C/Accession: A46328

R/Sakaguchi, T.; Toyoda, T.; Gotoh, B.; Innocencio, N.M.; Kuma, K.; Miyata, T.; Nagai, Y.

Virol. 169, 260-272, 1989

A/Title: Newcastle disease virus evolution. I. Multiple lineages defined by sequence vari

A/Reference number: A46328; MUID:89204897; PMID:2705297

A/Accession: A46328

A/Molecule type: mRNA

A/Residues: 1-616 <SAK>

A/Cross-references: GB:M24705; NID:g332329; PIDN:AAA46655.1; PID:g332330

C/Genetics:

A/Gene: HN

C/Superfamily: paramyxovirus hemagglutinin-neuraminidase

C/Keywords: glycoprotein; glycosidase; hemagglutinin; hydrolase; transmembrane protein

P:27-48/Domain: transmembrane #status predicted <TM>

P:119,341,433,481,538,600/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 95.8%; Score 2871; DB 1; Length 616;

Best Local Similarity 94.6%; Pred. No. 5,76-213;

Matches 546; Conservative 15; Mismatches 16; Indels 0; Gaps 0;

1 MDRAVSQVALENDERAKNTWRLIFRIALLITVTLATSVASLVSMGASTPSDLVGP 60

1 MDRAVSQVALENDERAKNTWRLIFRIALLITVTLATSVASLVSMGASTPSDLVGP 60

1 MDRAVSQVALENDERAKNTWRLIFRIALLITVTLATSVASLVSMGASTPSDLVGP 60

1 MDRAVSQVALENDERAKNTWRLIFRIALLITVTLATSVASLVSMGASTPSDLVGP 60

1 MDRAVSQVALENDERAKNTWRLIFRIALLITVTLATSVASLVSMGASTPSDLVGP 60

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1 MDRAVSQVALENDERAKNTWRLIFRIALLITVTLATSVASLVSMGASTPSDLVGP 60

1 MDRAVSQVALENDERAKNTWRLIFRIALLITVTLATSVASLVSMGASTPSDLVGP 60

C/Species: Newcastle disease virus

C/Date: 30-Jun-1989 #sequence\_revision 30-Jun-1989 #text\_change 16-Jun-2000

C/Accession: B29823

R/Millar, N.S.; Chambers, P.; Emerson, P.T.

J. Gen. Virol. 69, 613-620, 1988

A/Title: Nucleotide sequence of the fusion and haemagglutinin-neuraminidase glycoprotein

ns.

A/Reference number: A92799; MUID:88171450; PMID:3351479

A/Accession: B29823

A/Molecule type: mRNA

A/Residues: 1-616 <ML>

A/Cross-references: GB:D00243; NID:G222174; PIDN:BA00174.1; PID:G222176

C/Genetics:

A/Gene: HN

C/Superfamily: paramyxovirus hemagglutinin-neuraminidase

C/Keywords: glycoprotein; glycosidase; hemagglutinin; hydrolase; transmembrane protein

P:27-54/Domain: transmembrane #status predicted <TM>

P:119,341,433,481,538,600/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 95.5%; Score 2862; DB 1; Length 616;

Best Local Similarity 94.3%; Pred. No. 2,86-212;

Matches 544; Conservative 18; Mismatches 15; Indels 0; Gaps 0;

1 MDRAVSQVALENDERAKNTWRLIFRIALLITVTLATSVASLVSMGASTPSDLVGP 60

1 MDRAVSQVALENDERAKNTWRLIFRIALLITVTLATSVASLVSMGASTPSDLVGP 60

1 MDRAVSQVALENDERAKNTWRLIFRIALLITVTLATSVASLVSMGASTPSDLVGP 60

1 MDRAVSQVALENDERAKNTWRLIFRIALLITVTLATSVASLVSMGASTPSDLVGP 60

1 MDRAVSQVALENDERAKNTWRLIFRIALLITVTLATSVASLVSMGASTPSDLVGP 60

1 MDRAVSQVALENDERAKNTWRLIFRIALLITVTLATSVASLVSMGASTPSDLVGP 60

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1 MDRAVSQVALENDERAKNTWRLIFRIALLITVTLATSVASLVSMGASTPSDLVGP 60

1 MDRAVSQVALENDERAKNTWRLIFRIALLITVTLATSVASLVSMGASTPSDLVGP 60

1 MDRAVSQVALENDERAKNTWRLIFRIALLITVTLATSVASLVSMGASTPSDLVGP 60

1 MDRAVSQVALENDERAKNTWRLIFRIALLITVTLATSVASLVSMGASTPSDLVGP 60

1 MDRAVSQVALENDERAKNTWRLIFRIALLITVTLATSVASLVSMGASTPSDLVGP 60

1 MDRAVSQVALENDERAKNTWRLIFRIALLITVTLATSVASLVSMGASTPSDLVGP 60



A:Reference number: A46328; MUID:89204897; PMID:2705297  
A:Accession: C46328  
A:Molecule type: mRNA  
A:Residues: 1-616 <SAK>  
A:Cross-references: GB:M24707  
C:Genetics:  
A:Gene: HN  
C:Superfamily: paramyxovirus hemagglutinin-neuraminidase  
C:Keywords: glycoprotein; glycosidase; hemagglutinin; hydrolase; transmembrane protein  
F:27-48/Domain: transmembrane #status predicted <TM>  
F:119,341,433,481,538,600/Binding site: carbohydrate (asn) (covalent) #status predicted

Query Match 95.0%; Score 2849; DB 1; Length 616;  
Best Local Similarity 93.9%; Pred. No. 2.8e-211;  
Matches 542; Conservative 18; Mismatches 17; Indels 0; Gaps 0;

QY 1 MDRASQVLENDREAKNTWRLFRIALLLTVTLATSVASLYVSGASTPSDLVIGP 60  
DB 1 MDRASQVLENDREAKNTWRLFRIALLLTVTLATSVASLYVSGASTPSDLVIGP 60  
QY 61 TRISRAEKRITSALGSNDVDRIYKOYALBESPLALNTETIMATSLSYQINGANN 120  
DB 61 TRISRAEKRITSALGSNDVDRIYKOYALBESPLALNTETIMATSLSYQINGANN 120  
QY 121 SGWGAPHDHPDPIGGIGKELIVDNASDVTSFYPSAFQEHNFIPAPTTGSGCTRIPSFDM 180  
DB 121 SGWGAPHDHPDPIGGIGKELIVDNASDVTSFYPSAFQEHNFIPAPTTGSGCTRIPSFDM 180  
QY 181 SATRYCTHNVILSGCRDHS HQYLAAGVLTATGRIFPSTLRSLDTONKSCSV 240  
DB 181 SATRYCTHNVILSGCRDHS HQYLAAGVLTATGRIFPSTLRSLDTONKSCSV 240  
QY 241 SATPLGCDMLCSKYTEBEDYNSAVPTLMAHGRIGFPGQVHEKDLDTTLFEDWVANYP 300  
DB 241 SATPLGCDMLCSKYTEBEDYNSAVPTLMAHGRIGFPGQVHEKDLDTTLFEDWVANYP 300  
QY 301 GVGGGSFIDGRVWFSVYGGKLPNSPDTVOEGKYVIYKRYNDTCPEDDYQIRMAKSSYK 360  
DB 301 GVGGGSFIDGRVWFSVYGGKLPNSPDTVOEGKYVIYKRYNDTCPEDDYQIRMAKSSYK 360  
QY 361 PGRFGKRIQQAIIISIKVSTSLGEDPVLTVPNTVTLMGAGRIITVGTSHFLYORGSSY 420  
DB 361 PGRFGKRIQQAIIISIKVSTSLGEDPVLTVPNTVTLMGAGRIITVGTSHFLYORGSSY 420  
QY 421 FSPALLYPMYTNKATLHSPYTFNAFTRPGRSIPCOASARCPNSCVTVYDPPVLYR 480  
DB 421 FSPALLYPMYTNKATLHSPYTFNAFTRPGRSIPCOASARCPNSCVTVYDPPVLYR 480  
QY 481 NHTLRGVFGTMDSEQARLNPAFAVFDSTSRSTRIRVSSSTKAAVTTSTCFKVKTKTKT 540  
DB 481 NHTLRGVFGTMDSEQARLNPAFAVFDSTSRSTRIRVSSSTKAAVTTSTCFKVKTKTKT 540  
QY 541 YCLSLAIISNTLFGFRIIVPLIVEILKNDGVREARS 577  
DB 541 YCLSLAIISNTLFGFRIIVPLIVEILKNDGVREARS 577

RESULT 9  
B46328 hemagglutinin-neuraminidase (EC 3.2.1.-) - Newcastle disease virus (strain QNE/66)  
C:Species: Newcastle disease virus  
C:Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 18-Jun-1999  
C:Accession: B46328  
R:Sakaguchi, T.; Toyoda, T.; Gotoh, B.; Inocencio, N.M.; Kuma, K.; Miyata, T.; Nagai, Y.  
Virology 169, 260-272, 1989  
A:Title: Newcastle disease virus evolution. I. Multiple lineages defined by sequence var  
A:Reference number: A46328; MUID:89204897; PMID:2705297  
A:Accession: B46328  
A:Molecule type: mRNA  
A:Residues: 1-616 <SAK>  
A:Cross-references: GB:M24706; NID:9332331; PID:AAA46654.1; PID:9332332  
C:Genetics:  
A:Gene: HN

C:Superfamily: paramyxovirus hemagglutinin-neuraminidase  
C:Keywords: glycoprotein; glycosidase; hemagglutinin; hydrolase; transmembrane protein  
F:27-48/Domain: transmembrane #status predicted <TM>  
F:119,341,433,481,538,600/Binding site: carbohydrate (asn) (covalent) #status predicted

Query Match 95.0%; Score 2848; DB 1; Length 616;  
Best Local Similarity 94.1%; Pred. No. 3.3e-211;  
Matches 542; Conservative 16; Mismatches 18; Indels 0; Gaps 0;

QY 1 MDRASQVLENDREAKNTWRLFRIALLLTVTLATSVASLYVSGASTPSDLVIGP 60  
DB 1 MDRASQVLENDREAKNTWRLFRIALLLTVTLATSVASLYVSGASTPSDLVIGP 60  
QY 61 TRISRAEKRITSALGSNDVDRIYKOYALBESPLALNTETIMATSLSYQINGANN 120  
DB 61 TRISRAEKRITSALGSNDVDRIYKOYALBESPLALNTETIMATSLSYQINGANN 120  
QY 121 SGWGAPHDHPDPIGGIGKELIVDNASDVTSFYPSAFQEHNFIPAPTTGSGCTRIPSFDM 180  
DB 121 SGWGAPHDHPDPIGGIGKELIVDNASDVTSFYPSAFQEHNFIPAPTTGSGCTRIPSFDM 180  
QY 181 SATRYCTHNVILSGCRDHS HQYLAAGVLTATGRIFPSTLRSLDTONKSCSV 240  
DB 181 SATRYCTHNVILSGCRDHS HQYLAAGVLTATGRIFPSTLRSLDTONKSCSV 240  
QY 241 SATPLGCDMLCSKYTEBEDYNSAVPTLMAHGRIGFPGQVHEKDLDTTLFEDWVANYP 300  
DB 241 SATPLGCDMLCSKYTEBEDYNSAVPTLMAHGRIGFPGQVHEKDLDTTLFEDWVANYP 300  
QY 301 GVGGGSFIDGRVWFSVYGGKLPNSPDTVOEGKYVIYKRYNDTCPEDDYQIRMAKSSYK 360  
DB 301 GVGGGSFIDGRVWFSVYGGKLPNSPDTVOEGKYVIYKRYNDTCPEDDYQIRMAKSSYK 360  
QY 361 PGRFGKRIQQAIIISIKVSTSLGEDPVLTVPNTVTLMGAGRIITVGTSHFLYORGSSY 420  
DB 361 PGRFGKRIQQAIIISIKVSTSLGEDPVLTVPNTVTLMGAGRIITVGTSHFLYORGSSY 420  
QY 421 FSPALLYPMYTNKATLHSPYTFNAFTRPGRSIPCOASARCPNSCVTVYDPPVLYR 480  
DB 421 FSPALLYPMYTNKATLHSPYTFNAFTRPGRSIPCOASARCPNSCVTVYDPPVLYR 480  
QY 481 NHTLRGVFGTMDSEQARLNPAFAVFDSTSRSTRIRVSSSTKAAVTTSTCFKVKTKTKT 540  
DB 481 NHTLRGVFGTMDSEQARLNPAFAVFDSTSRSTRIRVSSSTKAAVTTSTCFKVKTKTKT 540  
QY 541 YCLSLAIISNTLFGFRIIVPLIVEILKNDGVREARS 576  
DB 541 YCLSLAIISNTLFGFRIIVPLIVEILKNDGVREARS 576

RESULT 10  
HNNZOD hemagglutinin-neuraminidase (EC 3.2.1.-) precursor - Newcastle disease virus (strain Quee  
C:Species: Newcastle disease virus  
C:Date: 30-Sep-1989 #sequence\_revision 30-Sep-1989 #text\_change 18-Jun-1999  
C:Accession: A31110  
R:Gotman, V.J.; Nestorowicz, A.; Mitchell, S.J.; Corino, G.L.; Seliack, P.W.  
J. Biol. Chem. 263, 12522-12531, 1988  
A:Title: Characterization of the sites of proteolytic activation of Newcastle disease vi  
A:Reference number: A92665; MUID:88315049; PMID:3045120  
A:Accession: A31110  
A:Molecule type: genomic RNA  
A:Residues: 1-616 <GOK>  
A:Cross-references: GB:J03911; NID:9332327; PID:AAA46654.1; PID:9332328  
C:Genetics:  
A:Gene: HN  
C:Superfamily: paramyxovirus hemagglutinin-neuraminidase  
C:Keywords: glycoprotein; glycosidase; hemagglutinin; hydrolase; transmembrane protein  
F:1-574/Product: hemagglutinin-neuraminidase #status predicted <HNS>  
F:27-54/Domain: transmembrane #status predicted <TM>  
F:119,341,433,481,538,600/Binding site: carbohydrate (asn) (covalent) #status predicted

Query Match 94.9%; Score 2846; DB 1; Length 616;



QY 181 SATHYCYTHANVILSGCRDHSHQYALGVLRRTATGRIFFSTLRISLDDTONRKSCSV 240  
 DB 181 SATHYCYTHANVILSGCRDHSHQYALGVLRRTATGRIFFSTLRISLDDTONRKSCSV 240  
 QY 241 SATPLGCMCLSKYTEEREBEDYNASVPTLMAGLGFQGHEDLDVTLTPEBMANYP 300  
 DB 241 SATPLGCMCLSKYTEEREBEDYNASVPTLMAGLGFQGHEDLDVTLTPEBMANYP 300  
 QY 301 GVGGGSFIDGRWFSVYGLKPNPSPTVQEGKYIYKRYNDTCPEDEDOYIRMAKSSYK 360  
 DB 301 GVGGGSFIDGRWFSVYGLKPNPSPTVQEGKYIYKRYNDTCPEDEDOYIRMAKSSYK 360  
 QY 361 PGRFGKRIOQAIISIKVSTSLGEDPVLTVPPNTVTLMAGRGLTVGTSHPFYORGSSY 420  
 DB 361 PGRFGKRIOQAIISIKVSTSLGEDPVLTVPPNTVTLMAGRGLTVGTSHPFYORGSSY 420  
 QY 421 FSPALLYPMYVNNKTATLHSPYTFNAFTPFGSIPCOASARCPNSCVTVYDPPYLFYR 480  
 DB 421 FSPALLYPMYVNNKTATLHSPYTFNAFTPFGSIPCOASARCPNSCVTVYDPPYLFYR 480  
 QY 481 NHTLRGVFGTMDSEORALNPASAVFDSTSRRTITRVSSSTKAAYTSTGFKVKTNT 540  
 DB 481 NHTLRGVFGTMDSEORALNPASAVFDSTSRRTITRVSSSTKAAYTSTGFKVKTNT 540  
 QY 541 YCLSIABISNTLFGSEFRIVPLVLEILKNDGV 571  
 DB 541 YCLSIABISNTLFGSEFRIVPLVLEILKNDGV 571

## RESULT 13

hemagglutinin-neuraminidase (EC 3.2.1.-) - Newcastle disease virus

C:Species: Newcastle disease virus  
 C:Date: 31-Dec-1993 #sequence\_revision 22-Oct-1999 #text\_change 22-Oct-1999  
 C:Accession: S07126; B36829  
 R:Womers, C.D.; de Henau, S.; Neyt, C.; Bepion, D.; Letellier, C.; Meulemans, G.; Burny, Arch. Virol. 97, 101-113, 1987  
 A:Title: The hemagglutinin-neuraminidase (HN) gene of Newcastle disease virus strain Ita  
 A:Reference number: S07126; MUID:88076411; PMID:3318761  
 A:Accession: S07126  
 A:Molecule type: mRNA  
 A:Residues: 1-571 <MEM>  
 A:Cross-references: EMBL:M16640; NID:G332361; PIDN:AAA46671.1; PID:G332362  
 R:Sakaguchi, T.; Toyoda, T.; Gotoh, B.; Innocencio, N.M.; Kuma, K.; Miyata, T.; Nagai, Y. Virology 169, 260-272, 1989  
 A:Title: Newcastle disease virus evolution. I. Multiple lineages defined by sequence var  
 A:Reference number: A46328; MUID:89204897; PMID:2705297  
 A:Accession: B36829  
 A:Molecule type: mRNA  
 A:Residues: 1-2, 'UP', 5-52, 'S', 54-215, 'A', 217-399, 'AD', 402-571 <SAK>  
 A:Cross-references: GB:M24715  
 A:Experimental source: Strain ITA/45  
 C:Genetics: HN  
 C:Superfamily: paramyxovirus hemagglutinin-neuraminidase  
 C:Keywords: glycoprotein, glycosidase, hemagglutinin, hydrolase, transmembrane protein  
 F:27-48/Domain: transmembrane #status predicted <TM>  
 F:119,341,433,481,508,538/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match: 92.0%; Score 2758; DB 1; Length 571;

Best Local Similarity 91.1%; Pred. No. 2.6e-204; Indels 0; Gaps 0;

Matches 520; Conservative 25; Mismatches 26; Indels 0; Gaps 0;

QY 1 MDRASQVLENDEREAKNTWRLIFRIAILLLTVTLATSVASLVYSGASTPSDLVGP 60  
 DB 1 MDRASQVLENDEREAKNTWRLIFRIAILLLTVTLATSVASLVYSGASTPSDLVGP 60  
 QY 61 TRIRAEKITSALGSNDVVDRIYKQVLESPLALNTETTINMATISLSYQINGAANN 120  
 DB 61 TRIRAEKITSALGSNDVVDRIYKQVLESPLALNTETTINMATISLSYQINGAANN 120  
 QY 181 SATHYCYTHANVILSGCRDHSHQYALGVLRRTATGRIFFSTLRISLDDTONRKSCSV 240  
 DB 181 SATHYCYTHANVILSGCRDHSHQYALGVLRRTATGRIFFSTLRISLDDTONRKSCSV 240

QY 121 SGWAPLHDPDFIGGIGKEILVDNASDVTSFYPASFOEHLNFIAPPTGSGCTRIPEFDM 180  
 DB 121 SGWAPLHDPDFIGGIGKEILVDNASDVTSFYPASFOEHLNFIAPPTGSGCTRIPEFDM 180  
 QY 181 SATHYCYTHANVILSGCRDHSHQYALGVLRRTATGRIFFSTLRISLDDTONRKSCSV 240  
 DB 181 SATHYCYTHANVILSGCRDHSHQYALGVLRRTATGRIFFSTLRISLDDTONRKSCSV 240  
 QY 241 SATPLGCMCLSKYTEEREBEDYNASVPTLMAGLGFQGHEDLDVTLTPEBMANYP 300  
 DB 241 SATPLGCMCLSKYTEEREBEDYNASVPTLMAGLGFQGHEDLDVTLTPEBMANYP 300  
 QY 301 GVGGGSFIDGRWFSVYGLKPNPSPTVQEGKYIYKRYNDTCPEDEDOYIRMAKSSYK 360  
 DB 301 GVGGGSFIDGRWFSVYGLKPNPSPTVQEGKYIYKRYNDTCPEDEDOYIRMAKSSYK 360  
 QY 361 PGRFGKRIOQAIISIKVSTSLGEDPVLTVPPNTVTLMAGRGLTVGTSHPFYORGSSY 420  
 DB 361 PGRFGKRIOQAIISIKVSTSLGEDPVLTVPPNTVTLMAGRGLTVGTSHPFYORGSSY 420  
 QY 421 FSPALLYPMYVNNKTATLHSPYTFNAFTPFGSIPCOASARCPNSCVTVYDPPYLFYR 480  
 DB 421 FSPALLYPMYVNNKTATLHSPYTFNAFTPFGSIPCOASARCPNSCVTVYDPPYLFYR 480  
 QY 481 NHTLRGVFGTMDSEORALNPASAVFDSTSRRTITRVSSSTKAAYTSTGFKVKTNT 540  
 DB 481 NHTLRGVFGTMDSEORALNPASAVFDSTSRRTITRVSSSTKAAYTSTGFKVKTNT 540  
 QY 541 YCLSIABISNTLFGSEFRIVPLVLEILKNDGV 571  
 DB 541 YCLSIABISNTLFGSEFRIVPLVLEILKNDGV 571

## RESULT 14

hemagglutinin-neuraminidase (EC 3.2.1.-) - Newcastle disease virus (strain AUS/32)

C:Species: Newcastle disease virus  
 C:Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 15-Oct-1996  
 C:Accession: H46328  
 R:Sakaguchi, T.; Toyoda, T.; Gotoh, B.; Innocencio, N.M.; Kuma, K.; Miyata, T.; Nagai, Y. Virology 169, 260-272, 1989  
 A:Title: Newcastle disease virus evolution. I. Multiple lineages defined by sequence var  
 A:Reference number: A46328; MUID:89204897; PMID:2705297  
 A:Accession: H46328  
 A:Molecule type: mRNA  
 A:Residues: 1-571 <SAK>  
 A:Cross-references: GB:M24712  
 C:Genetics: HN  
 C:Superfamily: paramyxovirus hemagglutinin-neuraminidase  
 C:Keywords: glycoprotein, glycosidase, hemagglutinin, hydrolase, transmembrane protein  
 F:27-48/Domain: transmembrane #status predicted <TM>  
 F:119,341,433,481,508,538/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match: 91.8%; Score 2751; DB 1; Length 571;

Best Local Similarity 91.4%; Pred. No. 8.8e-204; Indels 0; Gaps 0;

Matches 522; Conservative 23; Mismatches 26; Indels 0; Gaps 0;

QY 1 MDRASQVLENDEREAKNTWRLIFRIAILLLTVTLATSVASLVYSGASTPSDLVGP 60  
 DB 1 MDRASQVLENDEREAKNTWRLIFRIAILLLTVTLATSVASLVYSGASTPSDLVGP 60  
 QY 61 TRIRAEKITSALGSNDVVDRIYKQVLESPLALNTETTINMATISLSYQINGAANN 120  
 DB 61 TRIRAEKITSALGSNDVVDRIYKQVLESPLALNTETTINMATISLSYQINGAANN 120  
 QY 121 SGWAPLHDPDFIGGIGKEILVDNASDVTSFYPASFOEHLNFIAPPTGSGCTRIPEFDM 180  
 DB 121 SGWAPLHDPDFIGGIGKEILVDNASDVTSFYPASFOEHLNFIAPPTGSGCTRIPEFDM 180  
 QY 181 SATHYCYTHANVILSGCRDHSHQYALGVLRRTATGRIFFSTLRISLDDTONRKSCSV 240  
 DB 181 SATHYCYTHANVILSGCRDHSHQYALGVLRRTATGRIFFSTLRISLDDTONRKSCSV 240



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OM protein - protein search, using sw model

Run on: January 2, 2004, 16:16:51 / Search time 19 Seconds  
(without alignments)  
1428.127 Million cell updates/sec

Title: US-09-915-515A-1

Perfect score: 2998  
Sequence: 1 MDRVSGVALENDERAKNT.....IVPLIVEILKNQGYEARSG 577

Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 127863 seqs, 47026705 residues  
Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database: SwissProt 41.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	2989	99.7	577 1 HEMA_NDV8	P32884 newcastle d
2	2938	98.0	577 1 HEMA_NDV8	P12553 newcastle d
3	2914	97.2	577 1 HEMA_NDV4	P12559 newcastle d
4	2913	97.2	577 1 HEMA_NDV1	P35743 newcastle d
5	2863	95.5	616 1 HEMA_NDV1	P12555 newcastle d
6	2862	95.5	616 1 HEMA_NDV1	P12558 newcastle d
7	2846	94.9	616 1 HEMA_NDV1	P12558 newcastle d
8	2763	92.2	571 1 HEMA_NDV3	P35741 newcastle d
9	2760	92.1	571 1 HEMA_NDV1	P12557 newcastle d
10	2758	92.0	571 1 HEMA_NDV1	P12554 newcastle d
11	2738.5	91.3	570 1 HEMA_NDV1	P35740 newcastle d
12	2711	90.4	571 1 HEMA_NDV1	P35742 newcastle d
13	2666	88.9	571 1 HEMA_NDV1	P25180 simian viru
14	838	28.0	571 1 HEMA_NDV1	P11235 mumps viru
15	781	26.1	582 1 HEMA_NDV1	P25466 human para
16	778	26.0	571 1 HEMA_NDV1	P25466 human para
17	777	25.9	571 1 HEMA_NDV1	P25466 human para
18	772	25.8	565 1 HEMA_NDV1	P25466 human para
19	771	25.7	565 1 HEMA_NDV1	P25466 human para
20	770	25.7	582 1 HEMA_NDV1	P10866 mumps viru
21	765	25.5	565 1 HEMA_NDV1	P25466 human para
22	765	25.5	565 1 HEMA_NDV1	P25466 human para
23	759	25.3	582 1 HEMA_NDV1	P25466 human para
24	689	23.0	573 1 HEMA_NDV1	P25466 human para
25	480	16.0	575 1 HEMA_NDV1	P25466 human para
26	479	16.0	575 1 HEMA_NDV1	P25466 human para
27	479	16.0	575 1 HEMA_NDV1	P25466 human para
28	469	15.6	575 1 HEMA_NDV1	P25466 human para
29	455.5	15.2	576 1 HEMA_NDV1	P25466 human para
30	448.5	15.0	576 1 HEMA_NDV1	P25466 human para
31	445.5	14.9	572 1 HEMA_NDV1	P25466 human para
32	444.5	14.8	572 1 HEMA_NDV1	P25466 human para
33	444	14.8	572 1 HEMA_NDV1	P25466 human para

34	441.5	14.7	572 1 HEMA_P13B	P06167 bovine para
35	441.5	14.7	572 1 HEMA_P13H	P12565 human para
36	441	14.7	572 1 HEMA_P13H	P12565 human para
37	439	14.6	572 1 HEMA_P13H	P12565 human para
38	433.5	14.5	575 1 HEMA_P13H	P16071 human para
39	145	4.8	1723 1 HEMA_P13H	P02812 chlamydia p
40	119	4.0	881 1 PRY3 YEAST	P47033 saccharomyc
41	118.5	4.0	5703 1 YN96 YEAST	P53753 saccharomyc
42	112	3.7	1117 1 YN96 YEAST	P53753 saccharomyc
43	111.5	3.7	773 1 CDH_BHACH	P01738 planerocoe
44	110	3.7	153 1 HEMA_MUMPS	P33480 mumps viru
45	109	3.6	670 1 YFGG_SCHPO	O13854 schizosacch

## ALIGNMENTS

RESULT 1  
HEMA\_NDV8 STANDARD; PRT; 577 AA.  
ID HEMA\_NDV8 P06158:  
AC P32884; P06158: 01-JAN-1988 (Rel. 06, Created)  
DT 01-JAN-1988 (Rel. 06, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Hemagglutinin-neuraminidase (EC 3.2.1.18).  
GN HN.  
OS Newcastle disease virus (strain Beaudette C/45) (NDV).  
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;  
OC Paramyxoviridae; Paramyxovirinae; Rubulaviruses.  
OX NCBI\_TaxID=11178;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=66306666; PubMed=3018130;  
RA Millar N.S., Chambers P., Emerson P.T.;  
RT "Nucleotide sequence analysis of the haemagglutinin-neuraminidase  
RT gene of Newcastle disease virus.";  
RL J. Gen. Virol. 67:1917-1927(1986).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=89204897; PubMed=2705297;  
RA Sakaguchi T., Toyoda T., Gotch B., Innocencio N.M., Kuma K., Miyata T.,  
RA Nagai Y.;  
RT "Newcastle disease virus evolution. I. Multiple lineages defined by  
RT sequence variability of the hemagglutinin-neuraminidase gene.";  
RL Virology 169:260-272(1989).  
CC -1- FUNCTION: HEMAGGLUTININ IS RESPONSIBLE FOR ATTACHING THE VIRUS  
CC TO CELL RECEPTORS AND FOR INITIATING INFECTION. NEURAMINIDASE  
CC ACTIVITY HELPS THE EFFICIENT SPREAD OF THE VIRUS BY DISSOCIATING  
CC THE NATURAL VIRIONS FROM THE NEURAMINIC ACID CONTAINING  
CC GLYCOPROTEINS.  
CC -1- CATALYTIC ACTIVITY: Hydrolysis of alpha-(2->3)-, alpha-(2->6)-,  
CC alpha-(2->8)-glycosidic linkages of terminal sialic residues in  
CC oligosaccharides, glycoproteins, glycolipids, colominic acid and  
CC synthetic substrates.  
CC -1- SUBCELLULAR LOCATION: EXTERNAL, ANCHORED TO THE ENVELOPE BY ITS  
CC N-TERMINAL HYDROPHOBIC SEQUENCE.  
CC -1- SIMILARITY: BELONGS TO THE PARAMYXOVIRUSES HEMAGGLUTININ-  
CC NEURAMINIDASE FAMILY.  
CC  
CC -----  
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CC or send an email to [license@ebi.ac.uk](mailto:license@ebi.ac.uk)).  
CC  
CC EMBL: X04355; CA27880.1; -;  
DR EMBL: M24710; AAA4660.1; -;  
DR EMBL: A03663; CA00289.1; -;  
DR PIR: F46328; F46328.  
DR InterPro: IPR000665; Hem-neuraminidase.  
DR Pfam: PF00423; HN; 1.

KW Hydrolyase; Hemagglutinin; Envelope protein; Glycoprotein;  
 KM Transmembrane.  
 FT MOD RES 1 1 BLOCKED.  
 FT DOMAIN 1 26 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 27 48 POTENTIAL.  
 FT DOMAIN 49 577 EXTRACELLULAR (POTENTIAL).  
 FT CARBOHYD 119 119 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 341 341 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 433 433 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 481 481 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 538 538 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 577 AA; 63142 MW; 1D4C52B487EC1A1 CRC64;  
 Query Match 99.7%; Score 2989; DB 1; Length 577;  
 Best Local Similarity 99.7%; Pred. No. 8.5e-229;  
 Matches 575; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 MDRASQVAVLENDERAKNTWRLIFRIALLTVTLATSVASLVSMGASTPSDVGIP 60  
 DB 1 MDRASQVAVLENDERAKNTWRLIFRIALLTVTLATSVASLVSMGASTPSDVGIP 60  
 QY 61 TRISRAEKTSLAGSNQDVVDRIYQVAVLESPALINTEETIMNATSLSQINGAANN 120  
 DB 61 TRISRAEKTSLAGSNQDVVDRIYQVAVLESPALINTEETIMNATSLSQINGAANN 120  
 QY 121 SGNGAPIHDPDFIGIGIKELIVNADSVTSFYPSAQEHNFIPAPTTSGGCTRIIPSDM 180  
 DB 121 SGNGAPIHDPDFIGIGIKELIVNADSVTSFYPSAQEHNFIPAPTTSGGCTRIIPSDM 180  
 QY 181 SATHYCYTHNVILSGCRDHS HQYALGVLTATGRIFFSTLRISLDDTONRKSQSV 240  
 DB 181 SATHYCYTHNVILSGCRDHS HQYALGVLTATGRIFFSTLRISLDDTONRKSQSV 240  
 QY 241 SATPLGCDMCSKYTEEDDYNSAVPTLMAHRLGDDGYHEKDLDTLLFEDWVANYP 300  
 DB 241 SATPLGCDMCSKYTEEDDYNSAVPTLMAHRLGDDGYHEKDLDTLLFEDWVANYP 300  
 QY 301 GVGGSFIDRWVPSVYVGLKPNSPDPTVEGKVIYKRYNDTCPEODYQIMAXSYK 360  
 DB 301 GVGGSFIDRWVPSVYVGLKPNSPDPTVEGKVIYKRYNDTCPEODYQIMAXSYK 360  
 QY 361 PGRFGKRIQOALLISKVSTSLGEDPVLTPVPTVTLMAGEGRILVGTSHFLYQSGSY 420  
 DB 361 PGRFGKRIQOALLISKVSTSLGEDPVLTPVPTVTLMAGEGRILVGTSHFLYQSGSY 420  
 QY 421 FSPALLYPMVSVKNTATLHSPYTNATRRGSI PCQASACPNSCVTGVYTDYPLFYR 480  
 DB 421 FSPALLYPMVSVKNTATLHSPYTNATRRGSI PCQASACPNSCVTGVYTDYPLFYR 480  
 QY 481 NHTLRGVFGTMDSEQARLNPAFAFDSTSRSTTRVSSSTRAAYTTSTCFKVVKTNKT 540  
 DB 481 NHTLRGVFGTMDSEQARLNPAFAFDSTSRSTTRVSSSTRAAYTTSTCFKVVKTNKT 540  
 QY 541 YCLSIASISNTLFGFEFRIVPLVLEILKNDGVREARSG 577  
 DB 541 YCLSIASISNTLFGFEFRIVPLVLEILKNDGVREARSG 577  
 RESULT 2  
 HEMA\_NDVVG STANDARD; PRT; 577 AA.  
 AC P12553;  
 DT 01-OCT-1989 (Rel. 12, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Hemagglutinin-neuraminidase (EC 3.2.1.18).  
 GN HN.  
 OS Newcastle disease virus (strain Texas G.b./48) (NDV).  
 OC Viruses; ssRNA negative-strand viruses; Mononegavirales;  
 OC Paramyxoviridae; Paramyxovirinae; Rubulavirinae;  
 OC NCBI\_taxid=11189;  
 RP SEQUENCE FROM N.A.

RX MEDLINE=88265873; PubMed=3388773;  
 RA Schaper U.M., Fuller F.J., Ward M.D.W., Mehrotra Y., Stone H.O.,  
 RA Stripp B.R., de Buyscher E.V.;  
 RT "Nucleotide sequence of the envelope protein genes of a highly  
 RT virulent, neurotropic strain of Newcastle disease virus."  
 RL Virology 165:251-295(1988).  
 RL [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=89204897; PubMed=2705297;  
 RA Sakaguchi T., Toyoda T., Gotoh B., Innocencio N.M., Kuma K., Miyata T.,  
 RA Nagai Y.;  
 RT "Newcastle disease virus evolution. I. Multiple lineages defined by  
 RT sequence variability of the hemagglutinin-neuraminidase gene."  
 RL Virology 169:260-272(1989).  
 CC -1- FUNCTION: HEMAGGLUTININ IS RESPONSIBLE FOR ATTACHING THE VIRUS  
 CC TO CELL RECEPTORS AND FOR INITIATING INFECTION. NEURAMINIDASE  
 CC ACTIVITY HELPS THE EFFICIENT SPREAD OF THE VIRUS BY DISSOCIATING  
 CC THE MATURE VIRIONS FROM THE NEURAMINIC ACID CONTAINING  
 CC GLYCOPROTEINS.  
 CC -1- CATALYTIC ACTIVITY: Hydrolysis of alpha-(2-3)-, alpha-(2-6)-,  
 CC alpha-(2-8)-glycosidic linkages of terminal sialic residues in  
 CC oligosaccharides, glycoproteins, glycolipids, colominic acid and  
 CC synthetic substrates.  
 CC -1- SUBCELLULAR LOCATION: EXTERNAL, ANCHORED TO THE ENVELOPE BY ITS  
 CC N-TERMINAL HYDROPHOBIC SEQUENCE.  
 CC -1- SIMILARITY: BELONGS TO THE PARAMYXOVIRUS HEMAGGLUTININ-  
 CC NEURAMINIDASE FAMILY.  
 CC -----  
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 CC -----  
 DR EMBL; M21409; AAA46669.1; -;  
 DR EMBL; M24711; AAA46661.1; -;  
 DR InterPro: IPR000665; Hem-neuramndase.  
 DR Pfam: PF00423; HN; 1.  
 KW Hydrolyase; Hemagglutinin; Envelope protein; Glycoprotein;  
 KM Transmembrane.  
 FT MOD RES 1 1 BLOCKED.  
 FT DOMAIN 1 26 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 27 48 POTENTIAL.  
 FT DOMAIN 49 577 EXTRACELLULAR (POTENTIAL).  
 FT CARBOHYD 119 119 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 341 341 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 433 433 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 481 481 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 538 538 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CONFLICT 160 H -> L (IN REF. 2).  
 FT CONFLICT 332 E -> R (IN REF. 2).  
 SQ SEQUENCE 577 AA; 63275 MW; 75CC2A5255626140 CRC64;  
 Query Match 98.0%; Score 2938; DB 1; Length 577;  
 Best Local Similarity 97.9%; Pred. No. 9.2e-225;  
 Matches 565; Conservative 5; Mismatches 7; Indels 0; Gaps 0;  
 QY 1 MDRASQVAVLENDERAKNTWRLIFRIALLTVTLATSVASLVSMGASTPSDVGIP 60  
 DB 1 MDRASQVAVLENDERAKNTWRLIFRIALLTVTLATSVASLVSMGASTPSDVGIP 60  
 QY 61 TRISRAEKTSLAGSNQDVVDRIYQVAVLESPALINTEETIMNATSLSQINGAANN 120  
 DB 61 TRISRAEKTSLAGSNQDVVDRIYQVAVLESPALINTEETIMNATSLSQINGAANN 120  
 QY 121 SGNGAPIHDPDFIGIGIKELIVNADSVTSFYPSAQEHNFIPAPTTSGGCTRIIPSDM 180  
 DB 121 SGNGAPIHDPDFIGIGIKELIVNADSVTSFYPSAQEHNFIPAPTTSGGCTRIIPSDM 180  
 QY 181 SATHYCYTHNVILSGCRDHS HQYALGVLTATGRIFFSTLRISLDDTONRKSQSV 240  
 DB 181 SATHYCYTHNVILSGCRDHS HQYALGVLTATGRIFFSTLRISLDDTONRKSQSV 240

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QY 241 SATPLGCMGCSKVTETEEEDYNSAVPTLMAHGLGFGQYHEKDLDTTLFEDWVANYP 300
DB 241 SATPLGCMGCSKVTETEEEDYNSAVPTLMAHGLGFGQYHEKDLDTTLFEDWVANYP 300
QY 301 GVGGSFIDGRVWPSVYGLKPNPSDPTVOEGKYIYKRYNDTCDEBDYQIRAKSSYK 360
DB 301 GVGGSFIDGRVWPSVYGLKPNPSDPTVOEGKYIYKRYNDTCDEBDYQIRAKSSYK 360
QY 361 PGRFGKRIQOAILISIKVTSLSGEDPVLTPPNTVTLMGAGRILTVGTSHPFLYORGSSY 420
DB 361 PGRFGKRIQOAILISIKVTSLSGEDPVLTPPNTVTLMGAGRILTVGTSHPFLYORGSSY 420
QY 421 FSPALLYPMVTSNKTATLHSPYTENAFTFRPGSIPCOASARCPNSCVTGVTDPYPLIFR 480
DB 421 FSPALLYPMVTSNKTATLHSPYTENAFTFRPGSIPCOASARCPNSCVTGVTDPYPLIFR 480
QY 481 NHTLRGVGTMLDGEOARLNPAASAVFSDTSRSRITRVSSSTKAAVTTSTCFKVKTKNT 540
DB 481 NHTLRGVGTMLDGEOARLNPAASAVFSDTSRSRITRVSSSTKAAVTTSTCFKVKTKNT 540
QY 541 YCLSIASISNTLFGFRIPLVPLVEILKNDGVREARSG 577
DB 541 YCLSIASISNTLFGFRIPLVPLVEILKNDGVREARSG 577

RESULT 3
HEMA_NDVH4 STANDARD; PRT; 577 AA.
AC P12559; P06158;
DT 01-OCT-1989, (Rel. 12, Created)
DT 01-OCT-1989, (Rel. 12, Last sequence update)
DE 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hemagglutinin-neuraminidase (EC 3.2.1.18).
GN HN.
OS Newcastle disease virus (strain BI-Hitchner/47) (NDV).
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Paramyxoviridae; Paramyxovirinae; Rubulavirinae.
OX NCBI_Taxid=11181;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87122141; PubMed=3027962;
RA Jorgensen E.D., Collins P.L., Lomedico P.T.;
RT "Cloning and nucleotide sequence of Newcastle disease virus
hemagglutinin-neuraminidase mRNA: identification of a putative sialic
acid binding site."
RL Virology 156:12-24(1987).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=89204897; PubMed=2705297;
RA Sakaguchi T., Toyoda T., Gotoh B., Innocencio N.M., Kuma K., Miyata T.,
RA Nagai Y.;
RT "Newcastle disease virus evolution. I. Multiple lineages defined by
sequence variability of the hemagglutinin-neuraminidase gene."
RL Virology 169:260-272(1989).
CC -1- FUNCTION: HEMAGGLUTININ IS RESPONSIBLE FOR ATTACHING THE VIRUS
TO CELL RECEPTORS AND FOR INITIATING INFECTION. NEURAMINIDASE
ACTIVITY HELPS THE EFFICIENT SPREAD OF THE VIRUS BY DISSOCIATING
THE MATURE VIRIONS FROM THE NEURAMINIC ACID CONTAINING
GLYCOPROTEINS.
CC -1- CATALYTIC ACTIVITY: Hydrolysis of alpha-(2->3)-, alpha-(2->6)-,
alpha-(2->8)-glycosidic linkages of terminal sialic residues in
oligosaccharides, glycoproteins, glycolipids, colominic acid and
synthetic substrates.
CC -1- SUBCELLULAR LOCATION: EXTERNAL, ANCHORED TO THE ENVELOPE BY ITS
N-TERMINAL HYDROPHOBIC SEQUENCE.
CC -1- SIMILARITY: BELONGS TO THE PARAMYXOVIRUSES HEMAGGLUTININ-
NEURAMINIDASE FAMILY.
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DR EMBL; M16573; AAA46668.1; -.
DR EMBL; M24708; AAA46658.1; -.
DR PIR; A26355; HNNZNC.
DR InterPro; IPR000665; Hem-neuramndase.
DR Pfam; PF00423; HN; 1.
KW Hydroxylase; Hemagglutinin; Envelope protein; Glycoprotein;
KW Transmembrane.
FT DOMAIN 1 26
FT TRANSMEM 27 48
FT DOMAIN 49 577
FT CARBOHYD 119 119
FT CARBOHYD 341 341
FT CARBOHYD 433 433
FT CARBOHYD 481 481
FT CARBOHYD 538 538
FT CONFLICT 200 200
FT CONFLICT 203 203
FT CONFLICT 324 324
SQ SEQUENCE 577 AA; 63241 MW; A7BCF780A8FF70E CRC64;

Query Match 97.2%; Score 2914; DB 1; Length 577;
Best Local Similarity 96.7%; Pred. No. 7,3e-223;
Matches 558; Conservative 8; Mismatches 11; Indels 0; Gaps 0;

QY 1 MDRAVSOVALENDERREAKNTWRLIFRIAILLTVVTATSVASLYVSGASTPSDLVGP 60
DB 1 MDRAVSOVALENDERREAKNTWRLIFRIAILLTVVTATSVASLYVSGASTPSDLVGP 60
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DB 61 TRIRAEKRTSALGSDNODVDRIYKQVALESPLALNTETTNATSLSYOINGANN 120
QY 121 SGWGAIPHDPPIGIGIKELIVDNASDVTSPYPAFOEHLNFIAPPTGSGCTRIPSHDM 180
DB 121 SGWGAIPHDPPIGIGIKELIVDNASDVTSPYPAFOEHLNFIAPPTGSGCTRIPSHDM 180
QY 181 SATHYCYTHNVILSGCRDHS HQYLAIGVLRATATGRIPFSTLRSLDPTONRKS CV 240
DB 181 SATHYCYTHNVILSGCRDHS HQYLAIGVLRATATGRIPFSTLRSLDPTONRKS CV 240
QY 241 SATPLGCMGCSKVTETEEEDYNSAVPTLMAHGLGFGQYHEKDLDTTLFEDWVANYP 300
DB 241 SATPLGCMGCSKVTETEEEDYNSAVPTLMAHGLGFGQYHEKDLDTTLFEDWVANYP 300
QY 301 GVGGSFIDGRVWPSVYGLKPNPSDPTVOEGKYIYKRYNDTCDEBDYQIRAKSSYK 360
DB 301 GVGGSFIDGRVWPSVYGLKPNPSDPTVOEGKYIYKRYNDTCDEBDYQIRAKSSYK 360
QY 361 PGRFGKRIQOAILISIKVTSLSGEDPVLTPPNTVTLMGAGRILTVGTSHPFLYORGSSY 420
DB 361 PGRFGKRIQOAILISIKVTSLSGEDPVLTPPNTVTLMGAGRILTVGTSHPFLYORGSSY 420
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DB 421 FSPALLYPMVTSNKTATLHSPYTENAFTFRPGSIPCOASARCPNSCVTGVTDPYPLIFR 480
QY 481 NHTLRGVGTMLDGEOARLNPAASAVFSDTSRSRITRVSSSTKAAVTTSTCFKVKTKNT 540
DB 481 NHTLRGVGTMLDGEOARLNPAASAVFSDTSRSRITRVSSSTKAAVTTSTCFKVKTKNT 540
QY 541 YCLSIASISNTLFGFRIPLVPLVEILKNDGVREARSG 577
DB 541 YCLSIASISNTLFGFRIPLVPLVEILKNDGVREARSG 577

RESULT 4
HEMA_NDVH4 STANDARD; PRT; 577 AA.
AC P35743;
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DT 01-JUN-1994 (Rel. 29, Created)  
 DT 01-JUN-1994 (Rel. 29, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Hemagglutinin-neuraminidase (EC 3.2.1.18).  
 GN HN.  
 OS Newcastle disease virus (strain Lae/46) (NDV).  
 OC Viruses; ssRNA negative-strand viruses; Mononegavirales;  
 OC Paramyxoviridae; Paramyxovirinae; Rubulavirinae.  
 NCBI\_TaxID=11164;  
 RX MEDLINE=89204897; PubMed=2705297;  
 RA Sakauchi T., Toyoda T., Gotoh B., Innocencio N.M., Kuma K., Miyata T.,  
 Nagai Y.;  
 RT "Newcastle disease virus evolution. I. Multiple lineages defined by  
 RT sequence variability of the hemagglutinin-neuraminidase gene.";  
 RL Virology 169:260-272(1989).  
 CC -1- FUNCTION: HEMAGGLUTININ IS RESPONSIBLE FOR ATTACHING THE VIRUS  
 CC TO CELL RECEPTORS AND FOR INITIATING INFECTION. NEURAMINIDASE  
 CC ACTIVITY HELPS THE EFFICIENT SPREAD OF THE VIRUS BY DISSOCIATING  
 CC THE MATURE VIRIONS FROM THE NEURAMINIC ACID CONTAINING  
 CC GLYCOPROTEINS.  
 CC -1- CATALYTIC ACTIVITY: Hydrolysis of alpha-(2->3)-, alpha-(2->6)-,  
 CC alpha-(2->8)-glycosidic linkages of terminal sialic residues in  
 CC oligosaccharides, glycoproteins, glycolipids, colominic acid and  
 CC synthetic substrates.  
 CC -1- SUBCELLULAR LOCATION: EXTERNAL, ANCHORED TO THE ENVELOPE BY ITS  
 CC N-TERMINAL HYDROPHOBIC SEQUENCE.  
 CC -1- SIMILARITY: BELONGS TO THE PARAMYXOVIRUSES HEMAGGLUTININ-  
 CC NEURAMINIDASE FAMILY.  
 CC -----  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 CC EMBL: M24709; AAA46659.1; -.  
 CC PIR: E46328; E46328.  
 CC DR InterPro: IPR000665; Hem-neuramndse.  
 CC DR Pfam: PF00423; HN; 1.  
 CC KM Hydrolyase; Hemagglutinin; Envelope protein; Glycoprotein;  
 CC Transmembrane.  
 CC FT DOMAIN 1 26 CYTOPLASMIC (POTENTIAL).  
 CC FT TRANSMEM 27 48 POTENTIAL.  
 CC FT DOMAIN 49 577 EXTRACELLULAR (POTENTIAL).  
 CC FT CARBOHYD 119 119 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 CC FT CARBOHYD 341 341 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 CC FT CARBOHYD 433 433 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 CC FT CARBOHYD 481 481 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 CC FT CARBOHYD 538 538 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 CC FT CARBOHYD 310 310 S -> G (IN REF. 1; AAA46659).  
 CC FT CONFLICT 502 502 A -> T (IN REF. 1; AAA46659).  
 CC FT CONFLICT 577 577 A -> T (IN REF. 1; AAA46659).  
 CC SQ SEQUENCE 577 AA; 63209 MW; E9939C6A8240364A CRC64;  
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 CC Query Match 97.2%; Score 2913; DB 1; Length 577;  
 CC Best Local Similarity 96.9%; Pred. No. 8.8e-223;  
 CC Matches 559; Conservative 8; Mismatches 10; Indels 0; Gaps 0;  
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 CC DB 1 MDRASQVALENREKAKTWRLIFRIAILLTVTLATSVASIVYVSGASTSDVIGIP 60  
 CC QY 61 TRISRAEKTISALGSNOVDVRIYKQVALESPLALNTETITMAITSLSYQINGANN 120  
 CC DB 61 TRISRAEKTISALGSNOVDVRIYKQVALESPLALNTETITMAITSLSYQINGANN 120  
 CC QY 121 SGWGAETIHPDPIFGIGIKELIVDNASVYTSFYSARFQEHNFIPARTTSGGCTRIISFDM 180  
 CC DB 121 SGWGAETIHPDPIFGIGIKELIVDNASVYTSFYSARFQEHNFIPARTTSGGCTRIISFDM 180  
 CC QY 121 SGWGAETIHPDPIFGIGIKELIVDNASVYTSFYSARFQEHNFIPARTTSGGCTRIISFDM 180  
 CC DB 121 SGWGAETIHPDPIFGIGIKELIVDNASVYTSFYSARFQEHNFIPARTTSGGCTRIISFDM 180

QY 181 SATHYCYTHNVILSGCRDHSQVYALGVLTARTATGRIFSTLRISLSDTQNRKSCV 240  
 DB 181 SATHYCYTHNVILSGCRDHSQVYALGVLTARTATGRIFSTLRISLSDTQNRKSCV 240  
 QY 241 SATPLGCDMLCSKVETEEEDYNSAVPTLMAGRLGFDQYHKKLDVTLTLEDVYANP 300  
 DB 241 SATPLGCDMLCSKVETEEEDYNSAVPTLMAGRLGFDQYHKKLDVTLTLEDVYANP 300  
 QY 301 GVGGSFIDGRWFSYVGGGLKPNSPEDTVQEGGVYKRYNTPCPDEPDYQIRMAKSSYK 360  
 DB 301 GVGGSFIDGRWFSYVGGGLKPNSPEDTVQEGGVYKRYNTPCPDEPDYQIRMAKSSYK 360  
 QY 361 PGRFGKRIQQAHLISKYSTSLGDEPVLTPPNTYTLMGAEGRILTVGTSHPLYQSGSY 420  
 DB 361 PGRFGKRIQQAHLISKYSTSLGDEPVLTPPNTYTLMGAEGRILTVGTSHPLYQSGSY 420  
 QY 421 FSPALLYPTVSNKATLTHSPYTENAFTTPGSIPOQASARCNSCYTGYTDPYPLIFR 480  
 DB 421 FSPALLYPTVSNKATLTHSPYTENAFTTPGSIPOQASARCNSCYTGYTDPYPLIFR 480  
 QY 481 NHTLRGVFGTMLDSEQARLNPASAVFDSRSRITRVSSSTKAAYTSTCFKVVTKNT 540  
 DB 481 NHTLRGVFGTMLDSEQARLNPASAVFDSRSRITRVSSSTKAAYTSTCFKVVTKNT 540  
 QY 541 YCLSIABISNTLFGERRIVPLVLEIKNDGVREARSG 577  
 DB 541 YCLSIABISNTLFGERRIVPLVLEIKNDGVREARSG 577

RESULT 5  
 ID HEMA NDV STANDARD; PRT; 616 AA.  
 AC P1255;  
 DT 01-OCT-1989 (Rel. 12, Created)  
 DT 01-OCT-1989 (Rel. 12, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Hemagglutinin-neuraminidase (EC 3.2.1.18).  
 GN HN.  
 OS Newcastle disease virus (strain D26/76) (NDV).  
 OC Viruses; ssRNA negative-strand viruses; Mononegavirales;  
 OC Paramyxoviridae; Paramyxovirinae; Rubulavirinae.  
 NCBI\_TaxID=11180;  
 RX MEDLINE=89160043; PubMed=2450424;  
 RA Gotoh B., Sakauchi T., Nishikawa K., Innocencio N.M., Hamaguchi M.,  
 Toyoda T., Nagai Y.;  
 RT "Structural features unique to each of the three antigenic sites on  
 RT the hemagglutinin-neuraminidase protein of Newcastle disease virus.";  
 RL Virology 163:174-182(1988).  
 CC -----  
 CC RP SEQUENCE FROM N.A.  
 CC RX MEDLINE=89204897; PubMed=2705297;  
 CC RA Sakauchi T., Toyoda T., Gotoh B., Innocencio N.M., Kuma K., Miyata T.,  
 CC Nagai Y.;  
 CC RT "Newcastle disease virus evolution. I. Multiple lineages defined by  
 CC RT sequence variability of the hemagglutinin-neuraminidase gene.";  
 CC RL Virology 169:260-272(1989).  
 CC CC -1- FUNCTION: HEMAGGLUTININ IS RESPONSIBLE FOR ATTACHING THE VIRUS  
 CC TO CELL RECEPTORS AND FOR INITIATING INFECTION. NEURAMINIDASE  
 CC ACTIVITY HELPS THE EFFICIENT SPREAD OF THE VIRUS BY DISSOCIATING  
 CC THE MATURE VIRIONS FROM THE NEURAMINIC ACID CONTAINING  
 CC GLYCOPROTEINS.  
 CC -1- CATALYTIC ACTIVITY: Hydrolysis of alpha-(2->3)-, alpha-(2->6)-,  
 CC alpha-(2->8)-glycosidic linkages of terminal sialic residues in  
 CC oligosaccharides, glycoproteins, glycolipids, colominic acid and  
 CC synthetic substrates.  
 CC -1- SUBCELLULAR LOCATION: EXTERNAL, ANCHORED TO THE ENVELOPE BY ITS  
 CC N-TERMINAL HYDROPHOBIC SEQUENCE.  
 CC -1- SIMILARITY: BELONGS TO THE PARAMYXOVIRUSES HEMAGGLUTININ-  
 CC NEURAMINIDASE FAMILY.  
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DR EMBL; M19432; AAA46638.1; -  
DR EMBL; M24705; AAA46655.1; -  
DR PIR; A46328; A46328.  
DR InterPro; IPR000665; Hem-neuramidase.

DR Pfam; PF00423; HN; 1.  
KM Hydrolase; Hemagglutinin, Envelope protein; Glycoprotein;  
KW Transmembrane.

FT DOMAIN 1 26 CYTOPLASMIC (POTENTIAL).  
FT TRANSSEM 27 48 POTENTIAL.  
FT DOMAIN 49 616 EXTRACELLULAR (POTENTIAL).  
FT CARBOHYD 119 119 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 341 341 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 433 433 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 481 481 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 538 538 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 600 600 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CONFLICT 199 199 R -> H (IN REF. 2).  
SQ SEQUENCE 616 AA; 67680 MW; 2FDFF7785C5DA62AA CRC64;

Query Match 95.5%; Score 2863; DB 1; Length 616;  
Best Local Similarity 94.5%; Pred. No. 8.7e-219;  
Matches 545; Conservative 15; Mismatches 17; Indels 0; Gaps 0;

QY 1 MDRVSVQVLENDREKAKNTWRLIFRIALLTVTLATSVASLVSGASTPSDLVGP 60  
DB 1 MDRVSVQVLENDREKAKNTWRLIFRIALLTVTLATSVASLVSGASTPSDLVGP 60  
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DB 61 TALSRTSEKTSALGSNOVDVRIYKQVLESPLALNTETTMMATSLSTQINGAAN 120  
QY 121 SGWGAPFHDPDFIGIGIKELIVNADSVTSFYPAPQEHNFIPARTGSGCTPIPSFM 180  
DB 121 SGWGAPFHDPDFIGIGIKELIVNADSVTSFYPAPQEHNFIPARTGSGCTPIPSFM 180  
QY 181 SATHYCYTHNVILSGCRDHSHQYLAGVLTATGRIFFSTLRSLSDDTQNRKCSV 240  
DB 181 SATHYCYTHNVILSGCRDHSHQYLAGVLTATGRIFFSTLRSLSDDTQNRKCSV 240  
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DB 301 GVGGSFPIIDRGVWSVYGLKPNSPDVTQEGKVIYKRVNDTPDDODVDIRAKSSYK 360  
QY 361 PGRGGRKRIQOALISIKVSTSLGEDPVLTVPNTVTLMAGRIILTVTSHFLYQSGSY 420  
DB 361 PGRGGRKRIQOALISIKVSTSLGEDPVLTVPNTVTLMAGRIILTVTSHFLYQSGSY 420  
QY 421 FSPALLYPMVYSNTATLHSPYTNAFTPGSIPCOASARCPNSCVTVYTPYPIFYR 480  
DB 421 FSPALLYPMVYSNTATLHSPYTNAFTPGSIPCOASARCPNSCVTVYTPYPIFYR 480  
QY 481 NHTLRGVGMJLDEQARLNPAVPSSTSRITRVSSSSTKAYTSCCFKVKTKNT 540  
DB 481 NHTLRGVGMJLDEQARLNPAVPSSTSRITRVSSSSTKAYTSCCFKVKTKNT 540  
QY 541 YCLSIABISNTLFGFRIPLVLVEILKNDGVREARSG 577  
DB 541 YCLSIABISNTLFGFRIPLVLVEILKNDGVREARSG 577

RESULT 6  
HEMA\_NDVU

ID HEMA\_NDVU STANDARD; PRT; 616 AA.  
AC P12558;  
DT 01-OCT-1989 (Rel. 12, Created)  
DT 01-OCT-1989 (Rel. 12, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Hemagglutinin-neuraminidase (EC 3.2.1.18)..  
GN HN.  
OS Newcastle disease virus (strain Ulster/67) (NDV).  
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;  
OC Paramyxoviridae; Paramyxovirinae; Rubulaviruses.  
OX NCBI\_TaxID=11190;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=8817450; PubMed=3351479;  
RA Millar N.S., Chambers P., Emerson P.T.;  
RT "Nucleotide sequence of the fusion and haemagglutinin-neuraminidase  
RT glycoprotein genes of Newcastle disease virus, strain Ulster;  
RT molecular basis for variations in pathogenicity between strains."  
RN J. Gen. Virol. 69:613-620(1988).  
[2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=8816043; PubMed=2450424;  
RA Gotoh B., Sakaguchi T., Nishikawa K., Innocencio N.M., Hamaguchi M.,  
RA Toyoda T., Nagai Y.;  
RT "Structural features unique to each of the three antigenic sites on  
RT the hemagglutinin-neuraminidase protein of Newcastle disease virus."  
RL Virology 163:174-182(1988).  
[3]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=89204897; PubMed=2705297;  
RA Sakaguchi T., Toyoda T., Gotoh B., Innocencio N.M., Kuma K., Miyata T.,  
RA Nagai Y.;  
RT "Newcastle disease virus evolution. I. Multiple lineages defined by  
RT sequence variability of the hemagglutinin-neuraminidase gene."  
RL Virology 163:260-272(1989).  
CC -1- FUNCTION: HEMAGGLUTININ IS RESPONSIBLE FOR ATTACHING THE VIRUS  
CC TO CELL RECEPTORS AND FOR INITIATING INFECTION. NEURAMINIDASE  
CC ACTIVITY HELPS THE EFFICIENT SPREAD OF THE VIRUS BY DISSOCIATING  
CC THE MATURE VIRIONS FROM THE NEURAMINIC ACID CONTAINING  
CC GLYCOPROTEINS.  
CC -1- CATALYTIC ACTIVITY: Hydrolysis of alpha-(2->3)-, alpha-(2->6)-,  
CC alpha-(2->8)-glycosidic linkages of terminal sialic residues in  
CC oligosaccharides, glycoproteins, glycolipids, colominic acid and  
CC synthetic substrates.  
CC -1- SUBCELLULAR LOCATION: EXTERNAL, ANCHORED TO THE ENVELOPE BY ITS  
CC N-TERMINAL HYDROPHOBIC SEQUENCE.  
CC -1- SIMILARITY: BELONGS TO THE PARAMYXOVIRUSES HEMAGGLUTININ-  
CC NEURAMINIDASE FAMILY.  
CC  
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FT CARBOHYD 481 481 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 538 538 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 600 600 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CONFLICT 74 74 L -> S (IN REF. 2).  
 FT CONFLICT 74 74 L -> H (IN REF. 3).  
 FT CONFLICT 259 259 E -> K (IN REF. 2).  
 FT CONFLICT 438 438 L -> R (IN REF. 2).  
 FT CONFLICT 495 495 K -> E (IN REF. 2).  
 FT CONFLICT 555 555 EF -> GI (IN REF. 3).  
 SQ SEQUENCE 616 AA; 67590 MW; E70D67796FDDDA36 CRC64;

Query Match 95.5%; Score 2862; DB 1; Length 616;  
 Best Local Similarity 94.3%; Pred. No. 1e-217;

Matches 544; Conservative 18; Mismatches 15; Indels 0; Gaps 0;

QY 1 MDRASQVLENDEREAKNTWRLIFRIALLTLVVTATSVASLVYSGASTPSDVGIP 60  
 DB 1 MDRASQVLENDEREAKNTWRLIFRIALLTLVVTATSVASLVYSGASTPSDVGIP 60  
 QY 61 TRISRAEEKITSLAGSNQDVVDRIYKQVLESPLALNTETTIMAITSLSYQINGAANN 120  
 DB 61 TRISRAEEKITSLAGSNQDVVDRIYKQVLESPLALNTETTIMAITSLSYQINGAANS 120  
 QY 121 SGHGAPIHDPDFIGIGKELIVDNASDVTSFYPSAFQEHINFIAPPTGSGCTRIIPSDM 180  
 DB 121 SGHGAPIHDPDFIGIGKELIVDNASDVTSFYPSAFQEHINFIAPPTGSGCTRIIPSDM 180  
 QY 181 SAHYCTTHNVILISGCDHSHSHQYALAGYLRKTSATGRVFFSLHSINLDDTONRSCSV 240  
 DB 181 SAHYCTTHNVILISGCDHSHSHQYALAGYLRKTSATGRVFFSLHSINLDDTONRSCSV 240  
 QY 241 SATPLGCDMLCSKTEREEDYNSAVPTLMAHGLGPDGYHEKDLDTTLFEDWVANYP 300  
 DB 241 SATPLGCDMLCSKTEREEDYNSAVPTLMAHGLGPDGYHEKDLDTTLFEDWVANYP 300  
 QY 301 GVGGSFIDGRWPFVSYGGLKPNSSDTVQEGKVIYKRYNDTCPEQDYQIMAKSSYK 360  
 DB 301 GVGGSFIDGRWPFVSYGGLKPNSSDTVQEGKVIYKRYNDTCPEQDYQIMAKSSYK 360  
 QY 361 PGRFGGRIGQOALLISTVSTSLGSDPVLTPPMTVTLMAGEGVLTVGSHFLYQSGSSY 420  
 DB 361 PGRFGGRIGQOALLISTVSTSLGSDPVLTPPMTVTLMAGEGVLTVGSHFLYQSGSSY 420  
 QY 421 FSPALLYPMVSNKATILHSPTFNATRPQSIIPQOASACPNSCVGVTDYDPIFYR 480  
 DB 421 FSPALLYPMVSNKATILHSPTFNATRPQSIIPQOASACPNSCVGVTDYDPIFYR 480  
 QY 481 NHTLRGVFGTMDLSEQARLNPASAFEDSTSRSTRVSSSTRAAYTSTCFKVVKTNKT 540  
 DB 481 NHTLRGVFGTMDLSEQARLNPASAFEDSTSRSTRVSSSTRAAYTSTCFKVVKTNKT 540  
 QY 541 YCISIAEISNTLFGEPFIIVPLVILKNDGVRARSG 577  
 DB 541 YCISIAEISNTLFGEPFIIVPLVILKNDGVRARSG 577

RESULT 7

HEMA\_NDVQ STANDARD; PRT; 616 AA.

DT 01-JAN-1990 (Rel. 13, Created)  
 DT 01-JAN-1990 (Rel. 13, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Hemagglutinin-neuraminidase (EC 3.2.1.18).  
 GN HN.  
 OS Newcastle disease virus (strain Queensland/66) (NDV).  
 OC Viruses; ssRNA negative-strand viruses; Mononegavirales;  
 OC Paramyxoviridae; Paramyxovirinae; Rubulavirinae;  
 OC NCBI\_TaxID=11166;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=88315049; PubMed=3045120;  
 RA Gorman J.J., Nestorowicz A., Mitchell S.J., Corino G.L., Selleck P.W.;

RT "Characterization of the sites of proteolytic activation of Newcastle  
 RT disease virus membrane glycoprotein precursors.";  
 RL J. Biol. Chem. 263:12522-12531(1988).  
 RL [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=89204897; PubMed=2705297;  
 RA Sakaguchi T., Toyoda T., Gotoh B., Innocencio N.M., Kuma K., Miyata T.,  
 RA Nagai Y.;  
 RT "Newcastle disease virus evolution. I. Multiple lineages defined by  
 RT sequence variability of the hemagglutinin-neuraminidase gene.";  
 RL Virology, 169:260-272(1989).  
 CC -1- FUNCTION: HEMAGGLUTININ IS RESPONSIBLE FOR ATTACHING THE VIRUS  
 CC TO CELL RECEPTORS AND FOR INITIATING INFECTION. NEURAMINIDASE  
 CC ACTIVITY HELPS THE EFFICIENT SPREAD OF THE VIRUS BY DISSOCIATING  
 CC THE MATURE VIRIONS FROM THE NEURAMINIC ACID CONTAINING  
 CC GLYCOPROTEINS.  
 CC -1- CATALYTIC ACTIVITY: Hydrolysis of alpha-(2->3)-, alpha-(2->6)-,  
 CC alpha-(2->8)-glycosidic linkages of terminal sialic residues in  
 CC oligosaccharides, glycoproteins, glycolipids, colominic acid and  
 CC synthetic substrates.  
 CC -1- SUBCELLULAR LOCATION: EXTERNAL, ANCHORED TO THE ENVELOPE BY ITS  
 CC N-TERMINAL HYDROPHOBIC SEQUENCE.  
 CC -1- SIMILARITY: BELONGS TO THE PARAMYXOVIRUSES HEMAGGLUTININ-  
 CC NEURAMINIDASE FAMILY.  
 CC -----  
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 CC -----  
 DR EMBL: J03911; AAA4654.1; -  
 DR EMBL: M24706; AAA4656.1; -  
 DR PIR: A31110; HNNZQD.  
 DR PIR: B46328; B46328.  
 DR InterPro: IPR000665; Hem-neuramidae.  
 DR Pfam: PF00423; HN: 1.  
 KW Hydrolyase, Hemagglutinin, Envelope protein, Glycoprotein;  
 KW Transmembrane.  
 FT DOMAIN 1 26  
 FT TRANSMEM 27 48  
 FT POTENTIAL.  
 FT DOMAIN 49 616  
 FT CARBOHYD 119 119 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 341 341 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 433 433 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 481 481 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 538 538 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 600 600 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CONFLICT 87 87 O -> H (IN REF. 2).  
 FT CONFLICT 113 113 R -> Q (IN REF. 2).  
 FT CONFLICT 151 151 Y -> F (IN REF. 2).  
 FT CONFLICT 432 432 S -> G (IN REF. 2).  
 FT CONFLICT 495 495 K -> E (IN REF. 2).  
 SQ SEQUENCE 616 AA; 67656 MW; CBF556EB3B8C060F CRC64;

Query Match 94.9%; Score 2846; DB 1; Length 616;

Best Local Similarity 93.9%; Pred. No. 1.9e-217; Indels 0; Gaps 0;

Matches 541; Conservative 19; Mismatches 16; Indels 0; Gaps 0;

QY 1 MDRASQVLENDEREAKNTWRLIFRIALLTLVVTATSVASLVYSGASTPSDVGIP 60  
 DB 1 MDRASQVLENDEREAKNTWRLIFRIALLTLVVTATSVASLVYSGASTPSDVGIP 60  
 QY 61 TRISRAEEKITSLAGSNQDVVDRIYKQVLESPLALNTETTIMAITSLSYQINGAANN 120  
 DB 61 TRISRAEEKITSLAGSNQDVVDRIYKQVLESPLALNTETTIMAITSLSYQINGAANS 120  
 QY 121 SGHGAPIHDPDFIGIGKELIVDNASDVTSFYPSAFQEHINFIAPPTGSGCTRIIPSDM 180  
 DB 121 SGHGAPIHDPDFIGIGKELIVDNASDVTSFYPSAFQEHINFIAPPTGSGCTRIIPSDM 180

QY 181 SATHYCTHNVILSGCRDHSYOLALGVRTTATGRIFFSTLRISLDTONRKCSCV 240  
 DB 181 SATHYCTHNVILSGCRDHSYOLALGVRTTATGRIFFSTLRISLDTONRKCSCV 240  
 QY 241 SATPLGCDMLCSKYTEEBEDYNSAVPTLMAHGRGFGQYHEKDLDTTLPEDMVANYP 300  
 DB 241 SATPLGCDMLCSKYTEEBEDYNSAVPTLMAHGRGFGQYHEKDLDTTLPEDMVANYP 300  
 QY 301 GVGGGSPFDGRWVSVYGLKPNPSPTVQEGKYIYKRYNDTCPEDDYOIRMAKSSYK 360  
 DB 301 GVGGGSPFDGRWVSVYGLKPNPSPTVQEGKYIYKRYNDTCPEDDYOIRMAKSSYK 360  
 QY 361 PGRFGKRIQOALISIKVSTSLGEDPVLTPPNTVTLMAEGRLLTVGTSHFLYQSGSY 420  
 DB 361 PGRFGKRIQOALISIKVSTSLGEDPVLTPPNTVTLMAEGRLLTVGTSHFLYQSGSY 420  
 QY 421 FSPALLVPMYVSNKATLHSPYTFNAFTFRPSIPQOASARCPNSCVTVYDPPPLIYR 480  
 DB 421 FSPALLVPMYVSNKATLHSPYTFNAFTFRPSIPQOASARCPNSCVTVYDPPPLIYR 480  
 QY 481 NHTLRGVGTMLDSEQARLNPAFAVFDSTSRRTIRVSSSTKAAYTSTGPKVYKTKT 540  
 DB 481 NHTLRGVGTMLDSEQARLNPAFAVFDSTSRRTIRVSSSTKAAYTSTGPKVYKTKT 540  
 QY 541 YCLSIATISNTLFGFRIPLVPLVEILKNDGVREARS 576  
 DB 541 YCLSIATISNTLFGFRIPLVPLVEILKNDGVREARS 576

## RESULT 8

HEMA\_NDVH3 STANDARD; PRT; 571 AA.

AC P15741;

DT 01-JUN-1994 (Rel. 29, Created)

DT 01-JUN-1994 (Rel. 29, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Hemagglutinin-neuraminidase (EC 3.2.1.18).

HN.

OS Newcastle disease virus (strain Her/33) (NDV).

OC Viruses; ssRNA negative-strand viruses; Mononegavirales;

OC Paramyxoviridae; Paramyxovirinae; Rubulaviruses.

OC NCBI\_TaxID=1187;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=89204897; PubMed=2705297;

RA Sakaguchi T., Toyoda T., Gotoh B., Innocencio N.M., Kuma K., Miyata T.,

RA Nagai Y.;

RT "Newcastle disease virus evolution. I. Multiple lineages defined by

RT sequence variability of the hemagglutinin-neuraminidase gene.";

RL Virology 169;260-272(1989).

CC -1- FUNCTION: HEMAGGLUTININ IS RESPONSIBLE FOR ATTACHING THE VIRUS

CC TO CELL RECEPTORS AND FOR INITIATING INFECTION. NEURAMINIDASE

CC ACTIVITY HELPS THE EFFICIENT SPREAD OF THE VIRUS BY DISSOCIATING

CC THE NATURE VIRIONS FROM THE NEURAMINIC ACID CONTAINING

CC GLYCOPROTEINS.

CC -1- CATALYTIC ACTIVITY: Hydrolysis of alpha-(2->3)-, alpha-(2->6)-,

CC alpha-(2->8)-glycosidic linkages of terminal sialic residues in

CC oligosaccharides, glycoproteins, glycolipids, colominic acid and

CC synthetic substrates.

CC -1- SUBCELLULAR LOCATION: EXTERNAL, ANCHORED TO THE ENVELOPE BY ITS

CC N-TERMINAL HYDROPHOBIC SEQUENCE.

CC -1- SIMILARITY: BELONGS TO THE PARAMYXOVIRUSES HEMAGGLUTININ-

CC NEURAMINIDASE FAMILY.

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CC EMBL; M24714; AAA46664.1; -

DR PIR; A36829, A36829.  
 DR InterPro; IPR000665; Hem-neuramndse.  
 DR Pfam; PF00423; HN; 1.  
 KW Hydroxylase; Hemagglutinin; Envelope protein; Glycoprotein;  
 KW Transmembrane.  
 FT DOMAIN 1 26  
 FT TRANSMEM 27 48  
 FT DOMAIN 49 571  
 FT CARBOHYD 119 119  
 FT CARBOHYD 341 341  
 FT CARBOHYD 433 433  
 FT CARBOHYD 481 481  
 FT CARBOHYD 508 508  
 FT CARBOHYD 538 538  
 SQ SEQUENCE 571 AA; 62609 MW; 60EB6A508C8A1BF CRC64;

Query Match 92.2%; Score 2763; DB 1; Length 571;  
 Best Local Similarity 91.6%; Pred. No. 6.5e-211;  
 Matches 523; Conservative 24; Mismatches 24; Indels 0; Gaps 0;

QY 1 MDRVSOVLENDREBAKNTWRLIFRIALLITVTLATSVASLVYMGASTPDLVIGIP 60  
 DB 1 MDRVSRVLENERBAKNTWRFVRIALLITVTLAISAAVYSMEASTPDLVIGIP 60  
 QY 61 TRIGRAEKITSALGSNOVDVDRYKQVLESPLALINTETITNNATISLVSQINGAAN 120  
 DB 61 TVIRAEKITSALSNQVDVDRYKQVLESPLALINTESVINMALTISLVSQINGAAN 120  
 QY 121 SGKAPLHDPDFIGIGELIVDNASDVTSFYPSAFQEHNFIPAPTTGSGCTRIPSFDM 180  
 DB 121 SGCGAPYHDPDYGIGIGELIVDNASDVTSFYPSAFQEHNFIPAPTTGSGCTRIPSFDM 180  
 QY 121 SGCGAPYHDPDYGIGIGELIVDNASDVTSFYPSAFQEHNFIPAPTTGSGCTRIPSFDM 180  
 DB 181 SATHYCTHNVILSGCRDHSYOLALGVRTTATGRIFFSTLRISLDTONRKCSCV 240  
 QY 241 SATPLGCDMLCSKYTEEBEDYNSAVPTLMAHGRGFGQYHEKDLDTTLPEDMVANYP 300  
 DB 241 SATPLGCDMLCSKYTEEBEDYNSAVPTLMAHGRGFGQYHEKDLDTTLPEDMVANYP 300  
 QY 301 GVGGGSPFDGRWVSVYGLKPNPSPTVQEGKYIYKRYNDTCPEDDYOIRMAKSSYK 360  
 DB 301 GVGGGSPFDGRWVSVYGLKPNPSPTVQEGKYIYKRYNDTCPEDDYOIRMAKSSYK 360  
 QY 361 PGRFGKRIQOALISIKVSTSLGEDPVLTPPNTVTLMAEGRLLTVGTSHFLYQSGSY 420  
 DB 361 PGRFGKRIQOALISIKVSTSLGEDPVLTPPNTVTLMAEGRLLTVGTSHFLYQSGSY 420  
 QY 421 FSPALLVPMYVSNKATLHSPYTFNAFTFRPSIPQOASARCPNSCVTVYDPPPLIYR 480  
 DB 421 FSPALLVPMYVSNKATLHSPYTFNAFTFRPSIPQOASARCPNSCVTVYDPPPLIYR 480  
 QY 481 NHTLRGVGTMLDSEQARLNPAFAVFDSTSRRTIRVSSSTKAAYTSTGPKVYKTKT 540  
 DB 481 NHTLRGVGTMLDSEQARLNPAFAVFDSTSRRTIRVSSSTKAAYTSTGPKVYKTKT 540  
 QY 541 YCLSIATISNTLFGFRIPLVPLVEILKNDGV 571  
 DB 541 YCLSIATISNTLFGFRIPLVPLVEILKNDGV 571

## RESULT 9

HEMA\_NDVH3 STANDARD; PRT; 571 AA.

AC P15571;

DT 01-OCT-1989 (Rel. 12, Created)

DT 01-OCT-1989 (Rel. 12, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Hemagglutinin-neuraminidase (EC 3.2.1.18).

HN.

OS Newcastle disease virus (strain Miyadera/51) (NDV).

OC Viruses; ssRNA negative-strand viruses; Mononegavirales;

OC Paramyxoviridae; Paramyxovirinae; Rubulaviruses.

NCBI\_TaxID=11185;  
 (1) SEQUENCE FROM N.A.  
 MEDLINE=86160043; PubMed=2450424;  
 RA Gotoh B., Sakaguchi T., Nishikawa K., Innocencio N.M., Hamaguchi M.,  
 RA Toyoda T., Nagai Y.;  
 RT "Structural features unique to each of the three antigenic sites on  
 RT the hemagglutinin-neuraminidase protein of Newcastle disease virus";  
 RL Virology 163:174-182(1988).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 MEDLINE=89204897; PubMed=2705297;  
 RA Sakaguchi T., Toyoda T., Gotoh B., Innocencio N.M., Kuma K., Miyata T.,  
 RA Nagai Y.;  
 RT "Newcastle disease virus evolution. I. Multiple lineages defined by  
 RT sequence variability of the hemagglutinin-neuraminidase gene";  
 RL Virology 163:260-272(1989).  
 CC -1- FUNCTION: HEMAGGLUTININ IS RESPONSIBLE FOR ATTACHING THE VIRUS  
 CC TO CELL RECEPTORS AND FOR INITIATING INFECTION. NEURAMINIDASE  
 CC ACTIVITY HELPS THE EFFICIENT SPREAD OF THE VIRUS BY DISSOCIATING  
 CC THE MATURE VIRIONS FROM THE NEURAMINIC ACID CONTAINING  
 CC GLYCOPROTEINS.  
 CC -1- CATALYTIC ACTIVITY: Hydrolysis of alpha-(2->3)-, alpha-(2->6)-,  
 CC alpha-(2->8)-glycosidic linkages of terminal sialic residues in  
 CC oligosaccharides, glycoproteins, glycolipids, colominic acid and  
 CC synthetic substrates.  
 CC -1- SUBCELLULAR LOCATION: EXTERNAL, ANCHORED TO THE ENVELOPE BY ITS  
 CC N-TERMINAL HYDROPHOBIC SEQUENCE.  
 CC -1- SIMILARITY: BELONGS TO THE PARAMYXOVIRUSES HEMAGGLUTININ-  
 CC NEURAMINIDASE FAMILY.  
 CC -----  
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 CC -----  
 DR EMBL; M19479; AAA46674.1; -;  
 DR EMBL; M24713; AAA46663.1; -;  
 DR InterPro; IPR000665; Hem-neuramidase.  
 DR Pfam; PF00423; HN; 1.  
 KM Hydrolyase; Hemagglutinin; Envelope protein; Glycoprotein;  
 KM Transmembrane.  
 FT DOMAIN 1 26 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 27 48 POTENTIAL.  
 FT DOMAIN 49 571 EXTRACELLULAR (POTENTIAL).  
 FT CARBOHYD 119 119 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 341 341 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 433 433 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 481 481 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 508 508 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 538 538 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CONFLICT 167 167 T -> P (IN REF. 2).  
 SQ SEQUENCE 571 AA; 62522 MW; F2891CE5137937D5 CRC64;  
 Query Match 92.1%; Score 2760; DB 1; Length 571;  
 Best Local Similarity 91.6%; Pred. No. 1.e-210;  
 Matches 523; Conservative 22; Mismatches 26; Indels 0; Gaps 0;

QY 181 SATHYCYTHNVLISGCRDHSQVYALGVLTATGRIFFSTLRISLDDTQNRKSCSV 240  
 DB |||||  
 QY 241 SATPLCGDMLCSKVTETBEDYNSAVPTLMAHGRGFCQYHEKLDVTTLEEDWYANP 300  
 DB |||||  
 QY 241 SATPLCGDMLCSKVTETBEDYNSAVPTLMAHGRGFCQYHEKLDVTTLEEDWYANP 300  
 DB |||||  
 QY 301 GVGGSFFIDGRWVFSYGGALKPNSPDTVOEGEKVYKYKYNTPCPEDQYQIRMAKSSYK 360  
 DB |||||  
 QY 301 GVGGSFFIDGRWVFSYGGALKPNSPDTVOEGEKVYKYKYNTPCPEDQYQIRMAKSSYK 360  
 DB |||||  
 QY 361 PGRFGKRIQOAILSIKYSTSLGDEPVLTPPNTVTLMAEGRIITVGTSHFLYGRSSY 420  
 DB |||||  
 QY 361 PGRFGKRIQOAILSIKYSTSLGDEPVLTPPNTVTLMAEGRIITVGTSHFLYGRSSY 420  
 DB |||||  
 QY 421 FSPALYPTVTKATLTPPTTNAFTPGSIPQASARCRNSCTVGYTDPYPLIFR 480  
 DB |||||  
 QY 421 FSPALYPTVTKATLTPPTTNAFTPGSIPQASARCRNSCTVGYTDPYPLIFR 480  
 DB |||||  
 QY 481 NHTLRGVFGMLDSEQRALNPASAVDSTRSRITRVSSSTKAAYTSTCFKVVTKNT 540  
 DB |||||  
 QY 481 NHTLRGVFGMLDSEQRALNPASAVDSTRSRITRVSSSTKAAYTSTCFKVVTKNT 540  
 DB |||||  
 QY 541 YCLSIASISNTLFGERRIVPLVEIKNDGV 571  
 DB |||||  
 QY 541 YCLSIASISNTLFGERRIVPLVEIKNDGV 571  
 DB |||||  
 QY 541 YCLSIASISNTLFGERRIVPLVEIKNDGV 571  
 DB |||||  
 RESULT 10  
 ID HEMA NDVI STANDARD; PRT; 571 AA.  
 AC P12556;  
 DT 01-OCT-1989 (Rel. 12, Created)  
 DT 01-OCT-1989 (Rel. 12, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Hemagglutinin-neuraminidase (EC 3.2.1.18).  
 GN HN.  
 OS Newcastle disease virus (strain Italian/45) (NDV).  
 OC viruses; ssRNA negative-strand viruses; Mononegavirales;  
 OC Paramyxoviridae; Paramyxovirinae; Rubulavirinae.  
 OX NCBI\_TaxID=11182;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=88076411; PubMed=3318761;  
 RA Memers C.D., de Henau S., Neyt C., Espion D., Letellier C.,  
 RA Neulemans G., Bury A.;  
 RT "The hemagglutinin-neuraminidase (HN) gene of Newcastle disease virus  
 RT strain Italian (NDV Italian): comparison with HNs of other strains  
 RT and expression by a vaccinia recombinant.";  
 RL Arch. Virol. 97:101-113(1987).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=89204897; PubMed=2705297;  
 RA Sakaguchi T., Toyoda T., Gotoh B., Innocencio N.M., Kuma K., Miyata T.,  
 RA Nagai Y.;  
 RT "Newcastle disease virus evolution. I. Multiple lineages defined by  
 RT sequence variability of the hemagglutinin-neuraminidase gene";  
 RL Virology 163:260-272(1989).  
 CC -1- FUNCTION: HEMAGGLUTININ IS RESPONSIBLE FOR ATTACHING THE VIRUS  
 CC TO CELL RECEPTORS AND FOR INITIATING INFECTION. NEURAMINIDASE  
 CC ACTIVITY HELPS THE EFFICIENT SPREAD OF THE VIRUS BY DISSOCIATING  
 CC THE MATURE VIRIONS FROM THE NEURAMINIC ACID CONTAINING  
 CC GLYCOPROTEINS.  
 CC -1- CATALYTIC ACTIVITY: Hydrolysis of alpha-(2->3)-, alpha-(2->6)-,  
 CC alpha-(2->8)-glycosidic linkages of terminal sialic residues in  
 CC oligosaccharides, glycoproteins, glycolipids, colominic acid and  
 CC synthetic substrates.  
 CC -1- SUBCELLULAR LOCATION: EXTERNAL, ANCHORED TO THE ENVELOPE BY ITS  
 CC N-TERMINAL HYDROPHOBIC SEQUENCE.  
 CC -1- SIMILARITY: BELONGS TO THE PARAMYXOVIRUSES HEMAGGLUTININ-  
 CC NEURAMINIDASE FAMILY.  
 CC -----

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CC EMBL; M18640; AAA46671.1; -  
 CC EMBL; M24715; AAA46665.1; -  
 CC PIR; S07126; B36829  
 CC InterPro; IPR000655; Hem-neuramidase.  
 CC Pfam; PF00423; HN; 1.  
 CC Hydrolase; Hemagglutinin; Envelope protein; Glycoprotein;  
 CC Transmembrane.

FT TRANSMEM 1 26 CYTOPLASMIC (POTENTIAL).  
 FT DOMAIN 27 48 POTENTIAL.  
 FT CARBOHYD 49 571 EXTRACELLULAR (POTENTIAL).  
 FT CARBOHYD 119 119 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 341 341 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 433 433 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 481 481 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 508 508 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 538 538 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CONFLICT 3 4 RA -> LP (IN REF. 2).  
 FT CONFLICT 52 52 T -> S (IN REF. 2).  
 FT CONFLICT 75 75 S -> G (IN REF. 2).  
 FT CONFLICT 216 216 T -> A (IN REF. 2).  
 FT CONFLICT 400 401 PE -> AD (IN REF. 2).  
 FT SEQUENCE 571 AA; 62604 MW; F1ECB12BEF46C00F CRC64;

Query Match 92.0%; Score 2758; DB 1; Length 571;  
 Best Local Similarity 91.1%; Pred. No. 1.6e-210;  
 Matches 520; Conservative 25; Mismatches 26; Indels 0; Gaps 0;

QY 1 MDRASQVLENDEREAKNTWRLIRIAILITVTLTASLVYSGASTPSDLVGIP 60  
 DB 1 MDRAGRAVALENEEREAQNTWRFRIAFILITITLISAALVYSEASTPSDGLVGIP 60  
 QY TRISAEEKITSAAGNDVDVRIKOVALBSPALMTETITMAITSLSQINGANN 120  
 DB TVISAEEKITSAAGNDVDVRIKOVALBSPALMTETITMAITSLSQINGANN 120  
 QY 121 SGWGPADHPDPIGIGELIYDNASDVTSFPSPAFQEHNLIPAPTTGSGGCTRIPSFDM 180  
 DB 121 SGCGAPVADPVIIGIGELIYDNASDVTSFPSPAFQEHNLIPAPTTGSGGCTRIPSFDM 180  
 QY 181 SATHYCYTHNVILSGCRDHSHQYLAGVLTATGRIPESTLRSISLDTQNRKSCSV 240  
 DB 181 SATHYCYTHNVILSGCRDHSHQYLAGVLTATGRIPESTLRSISLDTQNRKSCSV 240  
 QY 241 SATPIGCMGLGSKYTEBEDNSAVPTLMAGRIQFGQCHERKLDVTLPEDEVANYIP 300  
 DB 241 SATPIGCMGLGSKYTEBEDNSAVPTLMAGRIQFGQCHERKLDVTLPEDEVANYIP 300  
 QY 301 GVGGGSFIDGRVWFVYGGGLKPNSPDVQOEGKYIYKRYNDTCDEDDYOIRMAKSSYK 360  
 DB 301 GVGGGSFIDGRVWFVYGGGLKPNSPDVQOEGKYIYKRYNDTCDEDDYOIRMAKSSYK 360  
 QY 361 PGRFGKRIQQAIIISIKVSTISGEDPVLTPPNTVTLMGAGRIILVTGSHELYRGSSY 420  
 DB 361 PGRFGKRIQQAIIISIKVSTISGEDPVLTPPNTVTLMGAGRIILVTGSHELYRGSSY 420  
 QY 421 FSPALLYPMYTNKATLHSPPTNAFTRPGSIPOQASARCNSCVTVYDPIYLYR 480  
 DB 421 FSPALLYPMYTNKATLHSPPTNAFTRPGSIPOQASARCNSCVTVYDPIYLYR 480  
 QY 481 NHTLKGVTGMDSEQARLNPASAVFSDTSRRIYRVSSSSKAYATYSTGCKVYKTKT 540  
 DB 481 NHTLKGVTGMDSEQARLNPASAVFSDTSRRIYRVSSSSKAYATYSTGCKVYKTKT 540  
 QY 541 YCLSTAEISNTLFGFRIVPLLVLEILKNDGV 571  
 DB 541 YCLSTAEISNTLFGFRIVPLLVLEILKNDGV 571

DB 541 YCLSTAEISNTLFGFRIVPLLVLEILKNDGV 571  
 RESULT 11  
 ID HEMA\_NDVA STANDARD; PRT; 570 AA.  
 AC P12554;  
 DT 01-OCT-1989 (Rel. 12, Created)  
 DT 01-JUN-1994 (Rel. 29, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Hemagglutinin-neuraminidase (EC 3.2.1.18).  
 GN HN.  
 OS Newcastle disease virus (strain Australia-Victoria/32) (NDV).  
 OC Viruses; ssRNA negative-strand viruses; Mononegavirales;  
 OC Paramyxoviridae; Paramyxovirinae; Rubulavirus.  
 OX NCBI\_TaxID=11177;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=87266149; PubMed=3037818;  
 RA McGlimes L.W., Wilde A., Morrison T.G.;  
 RT "Nucleotide sequence of the gene encoding the Newcastle disease virus hemagglutinin-neuraminidase protein and comparisons of paramyxovirus hemagglutinin-neuraminidase protein sequences.";  
 RL Virus Res. 7:187-202 (1987).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=88315049; PubMed=3045120;  
 RA Gorman J.J., Nestorowicz A., Mitchell S.J., Corino G.L., Sellsack P.W.;  
 RT "Characterization of the sites of proteolytic activation of Newcastle disease virus membrane glycoprotein precursors.";  
 RL J. Biol. Chem. 263:12522-12531 (1988).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=89204897; PubMed=2705297;  
 RA Sakaguchi T., Toyoda T., Goton B., Innocencio N.M., Kuma K., Miyata T., Nagai Y.;  
 RT "Newcastle disease virus evolution. I. Multiple lineages defined by sequence variability of the hemagglutinin-neuraminidase gene.";  
 RL Virology 169:260-272 (1989).  
 CC - FUNCTION: HEMAGGLUTININ IS RESPONSIBLE FOR ATTACHING THE VIRUS TO CELL RECEPTORS AND FOR INITIATING INFECTION. NEURAMINIDASE ACTIVITY HELPS THE EFFICIENT SPREAD OF THE VIRUS BY DISSOCIATING THE MATURE VIRIONS FROM THE NEURAMINIC ACID CONTAINING GLYCOPROTEINS.  
 CC - CATALYTIC ACTIVITY: Hydrolysis of alpha-(2->3)-, alpha-(2->6)-, alpha-(2->8)-glycosidic linkages of terminal sialic residues in oligosaccharides, glycoproteins, glycolipids, colominic acid and synthetic substrates.  
 CC - SUBCELLULAR LOCATION: EXTERNAL, ANCHORED TO THE ENVELOPE BY ITS N-TERMINAL HYDROPHOBIC SEQUENCE.  
 CC - SIMILARITY: BELONGS TO THE PARAMYXOVIRUSES HEMAGGLUTININ-NEURAMINIDASE FAMILY.  
 CC -  
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FT CARBOHYD 432 432 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 480 480 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 507 507 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 537 537 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CONFLICT 184 184 H -> HY (IN REF. 3).  
 FT CONFLICT 197 197 D -> H (IN REF. 1).  
 FT CONFLICT 259 259 E -> Q (IN REF. 1).  
 SQ SEQUENCE 570 AA; 62284 MW; 96EFJPFED67179D7 CRC64;  
 Query Match 91.3%; Score 2738.5; DB 1; Length 570;  
 Best Local Similarity 91.2%; Pred. No. 5.6e-209;  
 Matches 521; Conservative 23; Mismatches 26; Indels 1; Gaps 1;  
 QY 1 MDRASQVLENDEREAKNTWRLIFRIAILLTVTATSVASIVSMGASTPSDVGIP 60  
 DB 1 MNRVAVQVLENDEREAKNTWRLVFRILAILLTVTALISAAALVSMGASTPSDVGIP 60  
 QY 61 TRISRAEKTSLAGSNQDVVDRIYKQVLESPLALNTETTMATISLSTQINGANN 120  
 DB 61 TRISRAEKTSLAGSNQDVVDRIYKQVLESPLALNTETTMATISLSTQINGANN 120  
 QY 121 SGNGAPIHDDPFIIGIGKEILIVDNASDVTSFYPSPAFQEHNFIPAPTTSGGCTRIIPSPDM 180  
 DB 121 SGNGAPIHDDPFIIGIGKEILIVDNASDVTSFYPSPAFQEHNFIPAPTTSGGCTRIIPSPDM 180  
 QY 181 SATHCYTNVILISGRDHSHQYALAGVLTATGRIFFSTLRSLSDDTQNRKSCSV 240  
 DB 181 SATH-CYTNVILISGRDHSHQYALAGVLTATGRIFFSTLRSLSDDTQNRKSCSV 239  
 QY 241 SATPLGCDMLCSKVTETEEDYNSAVPTLMAHGRIGDQYHEKDLDTTLFEDWVANYP 300  
 DB 240 SATPLGCDMLCSKVTETEEDYNSAVPTLMAHGRIGDQYHEKDLDTTLFEDWVANYP 299  
 QY 301 GVGGSFIDGRWFSYVGGKLPNSPDTVOEGKVIYKRNDCPCPDQYQIRMASSSYK 360  
 DB 300 GVGGSFIDGRWFSYVGGKLPNSPDTVOEGKVIYKRNDCPCPDQYQIRMASSSYK 359  
 QY 361 PGRFGGRKIQOAILSTKSTLSGEDPVLTPPNTVTLMAGEBRLTVGTSHPFYORSSY 420  
 DB 360 PGRFGGRKIQOAILSTKSTLSGEDPVLTPPNTVTLMAGEBRLTVGTSHPFYORSSY 419  
 QY 421 FSPALLYPMVSNKTATLHSPYTFNAFTRPGSIPCOASARCPNSCVTGYTDPYPLIFR 480  
 DB 420 FSPALLYPMVSNKTATLHSPYTFNAFTRPGSIPCOASARCPNSCVTGYTDPYPLIFR 479  
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 DB 480 NHTLRGVFGTMDSEQARLNPASAVPDSRSTRITRVSSTKAAYTTSCFPYVTKNT 539  
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 DB 540 YCLSIASISNTLFGEPRIVPLVEILKNDGV 570  
 RESULT 12  
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 AC P35740;  
 DT 01-JUN-1994 (Rel. 29, Created)  
 DT 01-JUN-1994 (Rel. 29, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Hemagglutinin-neuraminidase (EC 3.2.1.18).  
 GN HN.  
 OS Newcastle disease virus (strain Ch1/85) (NDV).  
 OC Viruses; ssRNA negative-strand viruses; Mononegavirales;  
 OC Paramyxoviridae; Paramyxovirinae; Rubulavirinae.  
 OX NCBI Taxid=11179;  
 RN 1;  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=89204897; Pubmed=2705297;  
 RA Sakaguchi T., Toyoda T., Gotch B., Innocencio N.M., Kuma K., Miyata T.,  
 Nagai Y.;  
 RT "Newcastle disease virus evolution. I. Multiple lineages defined by

RT sequence variability of the hemagglutinin-neuraminidase gene.";  
 RL Virology 169:260-272(1989).  
 CC -1- FUNCTION: HEMAGGLUTININ IS RESPONSIBLE FOR ATTACHING THE VIRUS  
 CC TO CELL RECEPTORS AND FOR INITIATING INFECTION. NEURAMINIDASE  
 CC ACTIVITY HELPS THE EFFICIENT SPREAD OF THE VIRUS BY DISSOCIATING  
 CC THE MATURE VIRIONS FROM THE NEURAMINIC ACID CONTAINING  
 CC GLYCOPROTEINS.  
 CC -1- CATALYTIC ACTIVITY: Hydrolysis of alpha-(2-3)-, alpha-(2-6)-,  
 CC alpha-(2-8)-glycosidic linkages of terminal sialic residues in  
 CC oligosaccharides, glycoproteins, glycolipids, colominic acid and  
 CC synthetic substrates.  
 CC -1- SUBCELLULAR LOCATION: EXTERNAL, ANCHORED TO THE ENVELOPE BY ITS  
 CC N-TERMINAL HYDROPHOBIC SEQUENCE.  
 CC -1- SIMILARITY: BELONGS TO THE PARAMYXOVIRUSES HEMAGGLUTININ-  
 CC NEURAMINIDASE FAMILY.  
 CC -----  
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 CC -----  
 DR EMBL; M24716; AAA46666.1; -;  
 DR PIR; C36829; C36829.  
 DR InterPro; IPR000665; Hem-neuramidae.  
 DR Pfam; PF00423; HN; 1.  
 KW Hydrolyase, Hemagglutinin, Envelope protein; Glycoprotein;  
 KW Transmembrane.  
 FT DOMAIN 1 26  
 FT TRANSMEM 27 48  
 FT DOMAIN 49 571  
 FT CARBOHYD 119 119 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 341 341 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 433 433 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 481 481 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 508 508 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 571 AA; 62901 MW; 3110CD668D71EF76 CRC64;  
 Query Match 90.4%; Score 2711; DB 1; Length 571;  
 Best Local Similarity 88.8%; Pred. No. 8.4e-207;  
 Matches 507; Conservative 32; Mismatches 32; Indels 0; Gaps 0;  
 QY 1 MDRASQVLENDEREAKNTWRLIFRIAILLTVTATSVASIVSMGASTPSDVGIP 60  
 DB 1 MNRVAVQVLENDEREAKNTWRLVFRILAILLTVTALISAAALVSMGASTPSDVGIP 60  
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 DB 61 TRISRAEKTSLAGSNQDVVDRIYKQVLESPLALNTETTMATISLSTQINGANN 120  
 QY 121 SGNGAPIHDDPFIIGIGKEILIVDNASDVTSFYPSPAFQEHNFIPAPTTSGGCTRIIPSPDM 180  
 DB 121 SGNGAPIHDDPFIIGIGKEILIVDNASDVTSFYPSPAFQEHNFIPAPTTSGGCTRIIPSPDM 180  
 QY 181 SATHCYTNVILISGRDHSHQYALAGVLTATGRIFFSTLRSLSDDTQNRKSCSV 240  
 DB 181 SATHCYTNVILISGRDHSHQYALAGVLTATGRIFFSTLRSLSDDTQNRKSCSV 240  
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 DB 241 SATPLGCDMLCSKVTETEEDYNSAVPTLMAHGRIGDQYHEKDLDTTLFEDWVANYP 300  
 QY 301 GVGGSFIDGRWFSYVGGKLPNSPDTVOEGKVIYKRNDCPCPDQYQIRMASSSYK 360  
 DB 301 GVGGSFIDGRWFSYVGGKLPNSPDTVOEGKVIYKRNDCPCPDQYQIRMASSSYK 360  
 QY 361 PGRFGGRKIQOAILSTKSTLSGEDPVLTPPNTVTLMAGEBRLTVGTSHPFYORSSY 420  
 DB 361 PGRFGGRKIQOAILSTKSTLSGEDPVLTPPNTVTLMAGEBRLTVGTSHPFYORSSY 420  
 QY 421 FSPALLYPMVSNKTATLHSPYTFNAFTRPGSIPCOASARCPNSCVTGYTDPYPLIFR 480





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CC synthetic substrates.
CC -1- SUBCELLULAR LOCATION: EXTERNAL, ANCHORED TO THE ENVELOPE BY ITS
CC N-TERMINAL HYDROPHOBIC SEQUENCE.
CC -1- SIMILARITY: BELONGS TO THE PARAMYXOVIRUSES HEMAGGLUTININ-
CC NEURAMINIDASE FAMILY.
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CC EMBL; M62733; AAA47451.1; -
CC EMBL; X64275; CAA45568.1; -
CC PIR; A36419; HNNZ41.
CC InterPro; IPR000665; Hem-neuramidae.
CC HydroLase; Hemagglutinin; Envelope protein; Glycoprotein;
CC Transmembrane.
CC DOMAIN 1 20 CYTOPLASMIC (POTENTIAL).
CC TRANSMEM 21 40 POTENTIAL.
CC DOMAIN 41 568 EXTRACELLULAR (POTENTIAL).
CC CARBOHYD 44 44 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CARBOHYD 111 111 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CARBOHYD 268 268 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CARBOHYD 280 280 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CARBOHYD 382 382 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CARBOHYD 513 513 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC SEQUENCE 568 AA; 61733 MW; 7C09738B2715F548 CRC64;
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Query Match 28.0%; Score 838; DB 1; Length 568;
Best Local Similarity 35.0%; Pred. No. 1.5e-58;
Matches 203; Conservative 103; Mismatches 220; Indels 54; Gaps 11;
QY 18 KNTWRLIFRIALLLVVTLATSVASL---VYSGASTPSDLVIGIPTRISAREKITSAL 74
DB 10 KRTFRAVFRLLITLITLIALSAALYEVTHNSNGSESNQVDFDTLNA---ITGNI 66
QY 75 GSNQDVDRIRYKQVALESPLALNTETTMATLSLSTQINGAANSGWAPHPDPEIG 134
DB 67 KSMIALNQILYNAAALPKIDSTESVLLAAKDLQFSPASQNCSSGGLNDLALYN 126
QY 135 GIGELILVNDASDVTSFYPSAFQEHNL---FIPAPTTGSGCTRPSPDMATHYCYTHN 191
DB 127 GINQYILSNSFAGTVGLGPL-----LNIPSFISATAPGCTRIPLSFSLTKTKMCTSHNV 181
QY 192 ILSCGRDHSHTOYALGLVLTATGRIFPSLTLSISLDDTONRKSCSVSATPLGCDMLC 251
DB 182 ILAGCADSKASNOYLAMGIVEQSADPEFRTMRTVLTLSGINRKSCSIVAFGGCALYC 241
QY 252 SKYTEFEEDYINAVPTLMHGRGFGQYH-----EKLDVTTLPEDVANTPGVGGGS 306
DB 242 YVATKTEQEDYAAATPSEL---RLTF---YYNETLVERTLTIPVVTGNMATLNPAGSGV 296
QY 307 FIDGRVWFVYGGGLKPSPDVQEGKYVLYKRYNDPCPEODQIUMASSYKPGFSG 366
DB 297 YHGYLAFFPYGGLIQAASAMNSQFSGYFLPQNPAYOCCSSAEQIUTAGSYVAMFSG 356
QY 367 KRIQOALISIKVSTLGEDEPVLTPPNTVTLMGAEGRILTVGSHFLYQSGSYFSPALL 426
DB 357 RLIGSAVLVCPILSDQQLDQCRVVLFNNSSETMGEGRLYTIGDLYYYQSSSMWTASLL 416
QY 427 Y-----PMTYSNKATITLHSPYTFNAFTPGSIPQOASARKCNSCVTGYDDPYR 475
DB 417 YKINTDFSGQLPLPIEAQWVPTYLVP-----RPGAQPSAGNFCPANCITGYADVMP 469
QY 476 LI-----FYRNHTLRGVFGTMLDSEQARLNPAAVDSRSLITVSSSSSTKAA 526
DB 470 KNNPFPAGSGGVNPNVPLFGAF---LWADYARVAVPTFYMASATQYKNTTGFPSNQGA 526
QY 527 TTSTCFKVVTKNTKYCLSLAIESNTLFGEPRIYVLVEIL 566
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DB 527 TTSTCFQNTGSKKIYCLFTIEMGSSIMSGEFOIVPFEIREVI 566
RESULT 15
ID HEMA_MUMPM STANDARD; PRT; 582 AA.
AC P11235;
DT 01-JUL-1989 (Rel. 11, Created)
DT 01-JUL-1989 (Rel. 11, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hemagglutinin-neuraminidase (EC 3.2.1.18).
GN HN.
OS Mumps virus (strain Miyahara vaccine).
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Paramyxoviridae; Paramyxovirinae; Rubulavirus.
OX NCBI_Taxid:11171;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89345175; PubMed=2762157;
RA Takeuchi K., Tanabayashi K., Hishiyama M., Yamada A., Sugitara A.;
RT "Cloning and sequencing of the haemagglutinin-neuraminidase gene of
RT mumps virus (Miyahara strain).";
RL Nucleic Acids Res. 17:5840-5840(1989).
CC -1- FUNCTION: HEMAGGLUTININ IS RESPONSIBLE FOR ATTACHING THE VIRUS
CC TO CELL RECEPTORS AND FOR INITIATING INFECTION. NEURAMINIDASE
CC ACTIVITY HELPS THE EFFICIENT SPREAD OF THE VIRUS BY DISSOCIATING
CC THE MATURE VIRIONS FROM THE NEURAMINIC ACID CONTAINING
CC GLYCOPROTEINS.
CC -1- CATALYTIC ACTIVITY: Hydrolysis of alpha-(2->3)-, alpha-(2->6)-,
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CC oligosaccharides, glycoproteins, glycolipids, colominic acid and
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CC -1- SUBCELLULAR LOCATION: EXTERNAL, ANCHORED TO THE ENVELOPE BY ITS
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CC -1- SIMILARITY: BELONGS TO THE PARAMYXOVIRUSES HEMAGGLUTININ-
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CC EMBL; X15284; CAA33358.1; -
CC PIR; A34054; HNNZM.
CC InterPro; IPR000665; Hem-neuramidae.
CC Pfam; PF00423; HN; 1.
CC HydroLase; Hemagglutinin; Envelope protein; Glycoprotein;
CC Transmembrane.
CC DOMAIN 1 34 CYTOPLASMIC (POTENTIAL).
CC TRANSMEM 35 53 MEMBRANE ANCHOR (POTENTIAL).
CC DOMAIN 54 582 EXTRACELLULAR (POTENTIAL).
CC CARBOHYD 127 127 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CARBOHYD 127 284 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CARBOHYD 329 329 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CARBOHYD 400 400 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CARBOHYD 448 448 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CARBOHYD 464 464 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CARBOHYD 507 507 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC SEQUENCE 582 AA; 64044 MW; 990260039625499 CRC64;
SQ
Query Match 26.1%; Score 781; DB 1; Length 582;
Best Local Similarity 33.8%; Pred. No. 5e-54;
Matches 194; Conservative 103; Mismatches 231; Indels 46; Gaps 15;
QY 18 KNTWRLIFRIALLLVVTLATSVASL---VYSGASTPSDLVIGIPTRISAREKITSAL 71
DB 26 KRTFRCPLRILSVQAVALLIVYTLGLVEMINDQGS--NQSLSDIKRESATMIA 83
QY 72 SALGSDQVDRIYKQVALESPLALNTETTMATLSL---SYQINGAANSGWAP-1 127
```



Db 84 SAVG---VMOQVHGVTVSLPLQIEGNQNOJLSTLATICGKXQVNSCSTN---IPLV 135  
QY 128 HDPFIIIGIGIKELIYDNAS-DVTSFYP3AFQEHIN--FIPAPTTGSGCTRIIPSPFMSAT 183  
Db 136 NDLRFINGINKEFIIEDYTHDFISGHP-----LMBPFIPTAISPNCTRIIPSPFLGKT 189  
QY 184 HCYTHNVILSGCRDHSHQYLALGVLRRTATGRIFPSTLRISLDDTQNRKSCSVSAT 243  
Db 190 HMCYTHNVINANCMDHTSSNOYISMGILVQTAGYPMFKTLKIQYLSGLNRKSCSIATV 249  
QY 244 PLGCDMLCSKYTEHEEDYNSAVPTLMAHGRIGFDQYHEKODVYTLFEDWVANYPGVG 303  
Db 250 PDGCAMCYVSTOLETDDYAGSSPPTQKLTLLFYNDYTERTISPTGLGNWATLVPGVG 309  
QY 304 GGSFIDGRVWFSVVGGLKPNPSDPTVOEGK--YVIYKRYNDTCPEODDYQIRMAKSSYKP 361  
Db 310 SGTYFENKLIIPAYGGVLPNS-SLGVSAREPFPVNPYPCSGPQDDLQOR-ALRSTYF 367  
QY 362 GRFGGKRIQOAILSLIKVSTSLGEDPVLTPPNTVTLMGAEGRIILVTGSHFLYQSGSSYF 421  
Db 368 SYFSNRVQSAFLVCAMNQIILVTNCELVPNSNQTLMGABGRVLLINNRLLYQGSTSW 427  
QY 422 SPALLYPM---TVSNKTATLHSPYTFNAFTRPGSIPQASARCPNSCVTGVYTDYPLI 477  
Db 428 PYELIYELISFTFTNSGQSSVMSWPIYSFTRPGSGNCGENVCPTACVSGVYLDPMPLT 487  
QY 478 FYRHHTLRGV-----FGTMLDSEQARLNPASAVPDSRSTRITRVSSSTKAAYTSTC 531  
Db 488 PYSHOS--GINRNFYFTGALLNSSTTRVNPFTLYVSALNNLKVLAEPYNGQLFASYYTTTC 545  
QY 532 FKVVYTNKTYCLSLAELISNTLFGEEFRIVPLVEI 565  
Db 546 FQDTGDASVYCVYIMELASNIYGEFQILPVLTRL 579

Search completed: January 2, 2004, 16:18:50  
Job time : 21 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 2, 2004, 16:16:52 ; Search time 62 Seconds  
(without alignments)  
2401.554 Million cell updates/sec

Title: US-09-915-515A-1

Perfect score: 2998  
Sequence: 1 MDRVSVQVALENDEREAKNT.....IVPLVETIKNDGVREARSG 577

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: SPTREMBL\_23.\*  
2: sp\_archaea.\*  
3: sp\_bacteria.\*  
4: sp\_fungi.\*  
5: sp\_human.\*  
6: sp\_invertebrate.\*  
7: sp\_mammal.\*  
8: sp\_mhc.\*  
9: sp\_organelle.\*  
10: sp\_plant.\*  
11: sp\_protent.\*  
12: sp\_virus.\*  
13: sp\_vertebrate.\*  
14: sp\_unclassified.\*  
15: sp\_virus.\*  
16: sp\_bacteriap.\*  
17: sp\_archaeap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2998	100.0	577	12	Q9Q2W5 newcastle d
2	2926	97.6	577	12	Q9W8Z8 newcastle d
3	2920	97.4	577	12	Q83846 newcastle d
4	2920	97.4	577	12	Q90340 newcastle d
5	2917	97.3	577	12	Q91U00 newcastle d
6	2915	97.2	577	12	Q91AH7 newcastle d
7	2915	97.2	577	12	Q8B9S0 newcastle d
8	2913	97.2	577	12	Q83842 newcastle d
9	2902	96.8	577	12	Q9W9H0 newcastle d
10	2897	96.6	577	12	Q8BA53 newcastle d
11	2887	96.3	577	12	Q83844 newcastle d
12	2887	96.3	577	12	Q83845 newcastle d
13	2886	96.3	577	12	Q9WCW3 newcastle d
14	2863	95.5	577	12	Q89712 newcastle d
15	2860	95.4	577	12	Q83843 newcastle d
16	2838	94.7	616	12	Q83852 newcastle d

17	2821.5	94.1	615	12	Q83758 newcastle d
18	2801	93.4	572	12	Q56978 newcastle d
19	2748	91.7	572	12	Q56979 newcastle d
20	2746	91.6	571	12	Q83851 newcastle d
21	2746	91.6	571	12	Q91HD4 newcastle d
22	2730	91.1	571	12	Q73489 newcastle d
23	2727	91.0	571	12	Q9YN79 newcastle d
24	2726	90.9	571	12	Q9W9B1 newcastle d
25	2720	90.7	571	12	Q93161 newcastle d
26	2719.5	90.7	581	12	Q83850 newcastle d
27	2712	90.5	571	12	Q9W9I9 newcastle d
28	2703	90.2	571	12	Q9PYA4 newcastle d
29	2702	90.1	571	12	Q73490 newcastle d
30	2690	89.7	571	12	Q914X2 newcastle d
31	2687	89.6	571	12	Q8V1R0 newcastle d
32	2685	89.6	571	12	Q8V1O8 newcastle d
33	2684	89.5	571	12	Q91249 newcastle d
34	2681	89.4	571	12	Q8V1R1 newcastle d
35	2680	89.4	571	12	Q8V1R2 newcastle d
36	2667	89.0	571	12	Q83848 newcastle d
37	2667	89.0	571	12	Q8V1O9 newcastle d
38	2663	88.8	571	12	Q838X7 newcastle d
39	2662	88.8	571	12	Q9QCN6 newcastle d
40	2661	88.8	571	12	Q9W129 newcastle d
41	2658	88.7	571	12	Q9W9C3 newcastle d
42	2654	88.5	571	12	Q73491 newcastle d
43	2648	88.3	571	12	Q9YN78 newcastle d
44	1262	42.1	254	12	Q9E1T1 newcastle d
45	978	32.6	228	12	Q8BBT7 newcastle d

#### ALIGNMENTS

##### RESULT 1

ID Q9Q2W5 PRELIMINARY; PRT; 577 AA.

AC Q9Q2W5;

DT 01-MAY-2000 (TREMBLrel. 13, Created)

DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)

DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)

DE Hemagglutinin-neuraminidase glycoprotein.

OS Newcastle disease virus.

OC Viruses; ssRNA negative-strand viruses; Mononegavirales;

OC Paramyxoviridae; Paramyxovirinae; Rubulavirus.

OX NCBI\_TaxID=11176;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=Kansas.

RX MEDLINE=20238045; PubMed=10772993;

RA Takimoto T., Taylor G.L., Crennell S.J., Scroggs R.A., Portner A.;

RT "Crystallization of Newcastle disease virus hemagglutinin-

RT neuraminidase glycoprotein."

RL Virology 270:208-214(2000).

DR EMBL; AF212323; AAF19984.1; -

DR InterPro: IPR000665; Hem-neuramndse.

DR Pfam; PF00423; HN; 1.63111 MW; 6A1F03C8DD3F7753 CRC64;

SQ SEQUENCE 577 AA; 63111 MW; 6A1F03C8DD3F7753 CRC64;

Query Match 100.0%; Score 2998; DB 12; Length 577;  
Best Local Similarity 100.0%; Pred. No. 1.9e-237;  
Matches 577; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MDRVSVQVALENDEREAKNTWRLIFRAILLLITVTLATSVASLVYSGASTPSDVLGIP	60
DB	1	MDRVSVQVALENDEREAKNTWRLIFRAILLLITVTLATSVASLVYSGASTPSDVLGIP	60
QY	61	TRISRAEKITSALGSDVDVDRIVYKQVALESPLALNTETTINNAITSSVQINGANN	120
DB	61	TRISRAEKITSALGSDVDVDRIVYKQVALESPLALNTETTINNAITSSVQINGANN	120
QY	121	SGMGAPTHDPFGIGIGIKELIVDNASDVTSFYPAPQEHILNFIAPPTGSGCTRIIPSGDM	180

Db 121 SGWGAIPHDDPFIIGIGKELIVDNASDVTSFYPSPAFQEHNLNIPAPTTGSGCTRIIPSPDM 180  
Qy 181 SATHYCYTHNVILSGCRDHSYQYALGVLTATATRIFFSTLRSLDDTONRKSCSV 240  
Db 181 SATHYCYTHNVILSGCRDHSYQYALGVLTATATRIFFSTLRSLDDTONRKSCSV 240  
Qy 241 SATPLGCDMLCSKVTETEEDYNSAVPTLMAHGRIGFDQYHEKLDVTLTFEDWVANYP 300  
Db 241 SATPLGCDMLCSKVTETEEDYNSAVPTLMAHGRIGFDQYHEKLDVTLTFEDWVANYP 300  
Qy 301 GVGGGSEFIDGRVWFSYGGGLKPNSSPDTVOEGKVIYKRYNDTCPEBODYQIRMAKSSYK 360  
Db 301 GVGGGSEFIDGRVWFSYGGGLKPNSSPDTVOEGKVIYKRYNDTCPEBODYQIRMAKSSYK 360  
Qy 361 PGRFGKRIQOAILSTIKVSTSLGDEPVLTPPMTVTLMAGBGRILTVGSHFLYORGSSY 420  
Db 361 PGRFGKRIQOAILSTIKVSTSLGDEPVLTPPMTVTLMAGBGRILTVGSHFLYORGSSY 420  
Qy 421 FSPALLYPMTVSNKATLHSPYTFNAFTRPDSIPCOASARCNSCVTVGYTDPYPLIFR 480  
Db 421 FSPALLYPMTVSNKATLHSPYTFNAFTRPDSIPCOASARCNSCVTVGYTDPYPLIFR 480  
Qy 481 NHTLRGVFGTMDSEQARLNIPASAVFDSTSRIRTRVSSSTKAAVTTSTCFKVVTKNT 540  
Db 481 NHTLRGVFGTMDSEQARLNIPASAVFDSTSRIRTRVSSSTKAAVTTSTCFKVVTKNT 540  
Qy 541 YCLSTAEISNTLFGERRIVPLVEILKNDGVREARSG 577  
Db 541 YCLSTAEISNTLFGERRIVPLVEILKNDGVREARSG 577

## RESULT 2

Q9W8Z8 PRELIMINARY; PRT; 577 AA.  
AC Q9W8Z8;  
DT 01-NOV-1999 (TrEMBLrel. 12, Created)  
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)  
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)  
DE Hemagglutinin-neuraminidase.  
GN HN.  
OS Newcastle disease virus.  
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;  
OC Paramyxoviridae; Paramyxovirinae; Rubulaviruses.  
OX NCBI\_TaxId=11176;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=VACCINE-RUS LA SOTA TYPE);  
RA Gibanov O.G., Starov S.K., Lomakin A.I., Smolensky V.I., Drygin V.V.,  
RT "Phylogenetic analysis of Newcastle disease virus of Russia."  
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=VACCINE-RUS;  
RA Gibanov O.G., Starov S.K., Lomakin A.I., Smolensky V.I., Drygin V.V.,  
RT "Phylogenetic analysis of Newcastle disease virus of Russia."  
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP SEQUENCE FROM N.A.  
RC STRAIN=VACCINE-RUS;  
RA Gibanov O.G., Starov S.K., Lomakin A.I., Smolensky V.I., Drygin V.V.,  
RT "Phylogenetic analysis of Newcastle disease virus of Russia."  
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.  
EMBL: Y19020; CAB50911.1; -  
EMBL: Y19020; CAB50911.1; -  
EMBL: A1243386; CAB46067.1; -  
DR InterPro: IPR000665; Hem-neuramndse.  
DR Pfam: PF00423; HN; 1.  
SQ SEQUENCE 577 AA; 63153 MW; D4FCB45ECBDB089 CRC64;

Query Match 97.6%; Score 2926; DB 12; Length 577;

Best Local Similarity 97.2%; Pred. No. 1.6e-231;  
Matches 561; Conservative 9; Mismatches 7; Indels 0; Gaps 0;

Qy 1 MRAVSQVLENDERAKNTWRLIFRIATLLTVTLATSVASIVSMGASTPSPDVGP 60  
Db 1 MRAVSQVLENDERAKNTWRLIFRIATLLTVTLATSVASIVSMGASTPSPDVGP 60  
Qy 61 TRISRAEEKITSGNQDVNDRIYKQVALESPALLNTEETIMATLSIQINGAANN 120  
Db 61 TRISRAEEKITSGNQDVNDRIYKQVALESPALLNTEETIMATLSIQINGAANN 120  
Qy 121 SGWGAIPHDDPFIIGIGKELIVDNASDVTSFYPSPAFQEHNLNIPAPTTGSGCTRIIPSPDM 180  
Db 121 SGWGAIPHDDPFIIGIGKELIVDNASDVTSFYPSPAFQEHNLNIPAPTTGSGCTRIIPSPDM 180  
Qy 181 SATHYCYTHNVILSGCRDHSYQYALGVLTATATRIFFSTLRSLDDTONRKSCSV 240  
Db 181 SATHYCYTHNVILSGCRDHSYQYALGVLTATATRIFFSTLRSLDDTONRKSCSV 240  
Qy 241 SATPLGCDMLCSKVTETEEDYNSAVPTLMAHGRIGFDQYHEKLDVTLTFEDWVANYP 300  
Db 241 SATPLGCDMLCSKVTETEEDYNSAVPTLMAHGRIGFDQYHEKLDVTLTFEDWVANYP 300  
Qy 301 GVGGGSEFIDGRVWFSYGGGLKPNSSPDTVOEGKVIYKRYNDTCPEBODYQIRMAKSSYK 360  
Db 301 GVGGGSEFIDGRVWFSYGGGLKPNSSPDTVOEGKVIYKRYNDTCPEBODYQIRMAKSSYK 360  
Qy 361 PGRFGKRIQOAILSTIKVSTSLGDEPVLTPPMTVTLMAGBGRILTVGSHFLYORGSSY 420  
Db 361 PGRFGKRIQOAILSTIKVSTSLGDEPVLTPPMTVTLMAGBGRILTVGSHFLYORGSSY 420  
Qy 421 FSPALLYPMTVSNKATLHSPYTFNAFTRPDSIPCOASARCNSCVTVGYTDPYPLIFR 480  
Db 421 FSPALLYPMTVSNKATLHSPYTFNAFTRPDSIPCOASARCNSCVTVGYTDPYPLIFR 480  
Qy 481 NHTLRGVFGTMDSEQARLNIPASAVFDSTSRIRTRVSSSTKAAVTTSTCFKVVTKNT 540  
Db 481 NHTLRGVFGTMDSEQARLNIPASAVFDSTSRIRTRVSSSTKAAVTTSTCFKVVTKNT 540  
Qy 541 YCLSTAEISNTLFGERRIVPLVEILKNDGVREARSG 577  
Db 541 YCLSTAEISNTLFGERRIVPLVEILKNDGVREARSG 577

## RESULT 3

Q83846 PRELIMINARY; PRT; 577 AA.  
AC Q83846;  
DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)  
DE Hemagglutinin-neuraminidase.  
GN HN.  
OS Newcastle disease virus.  
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;  
OC Paramyxoviridae; Paramyxovirinae; Rubulaviruses.  
OX NCBI\_TaxId=11176;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=B1 (SBPR);  
RA Seal B.S., King D.J., Bennett J.D.;  
RT "Characterization of Newcastle disease virus vaccines by biological  
RT properties and sequence analysis of the hemagglutinin-neuraminidase  
RT protein gene."  
RL Vaccine 14:761-766 (1996).  
EMBL: U37193; AAC5047.1; -  
DR InterPro: IPR000665; Hem-neuramndse.  
DR Pfam: PF00423; HN; 1.  
SQ SEQUENCE 577 AA; 63215 MW; 866FA85D3A865404 CRC64;

Query Match 97.4%; Score 2920; DB 12; Length 577;  
Best Local Similarity 96.9%; Pred. No. 4.9e-231;  
Matches 559; Conservative 8; Mismatches 10; Indels 0; Gaps 0;

QY	1	MDRAVSQVAL	ENDEREAK	TKTWRLIF	IFPIALIL	TLVTWTLA	TSVSLV	SYNSGAST	PSPLVGP	60
Dd	1	MDRAVSQVAL <td>ENDEREAK<td>TKTWRLIF<td>IFPIALIL<td>TLVTWTLA<td>TSVSLV<td>SYNSGAST<td>PSPLVGP<td>60</td></td></td></td></td></td></td></td>	ENDEREAK <td>TKTWRLIF<td>IFPIALIL<td>TLVTWTLA<td>TSVSLV<td>SYNSGAST<td>PSPLVGP<td>60</td></td></td></td></td></td></td>	TKTWRLIF <td>IFPIALIL<td>TLVTWTLA<td>TSVSLV<td>SYNSGAST<td>PSPLVGP<td>60</td></td></td></td></td></td>	IFPIALIL <td>TLVTWTLA<td>TSVSLV<td>SYNSGAST<td>PSPLVGP<td>60</td></td></td></td></td>	TLVTWTLA <td>TSVSLV<td>SYNSGAST<td>PSPLVGP<td>60</td></td></td></td>	TSVSLV <td>SYNSGAST<td>PSPLVGP<td>60</td></td></td>	SYNSGAST <td>PSPLVGP<td>60</td></td>	PSPLVGP <td>60</td>	60
QY	1	MDRAVSQVAL <td>ENDEREAK<td>TKTWRLIF<td>IFPIALIL<td>TLVTWTLA<td>TSVSLV<td>SYNSGAST<td>PSPLVGP<td>60</td></td></td></td></td></td></td></td>	ENDEREAK <td>TKTWRLIF<td>IFPIALIL<td>TLVTWTLA<td>TSVSLV<td>SYNSGAST<td>PSPLVGP<td>60</td></td></td></td></td></td></td>	TKTWRLIF <td>IFPIALIL<td>TLVTWTLA<td>TSVSLV<td>SYNSGAST<td>PSPLVGP<td>60</td></td></td></td></td></td>	IFPIALIL <td>TLVTWTLA<td>TSVSLV<td>SYNSGAST<td>PSPLVGP<td>60</td></td></td></td></td>	TLVTWTLA <td>TSVSLV<td>SYNSGAST<td>PSPLVGP<td>60</td></td></td></td>	TSVSLV <td>SYNSGAST<td>PSPLVGP<td>60</td></td></td>	SYNSGAST <td>PSPLVGP<td>60</td></td>	PSPLVGP <td>60</td>	60
Dd	1	MDRAVSQVAL <td>ENDEREAK<td>TKTWRLIF<td>IFPIALIL<td>TLVTWTLA<td>TSVSLV<td>SYNSGAST<td>PSPLVGP<td>60</td></td></td></td></td></td></td></td>	ENDEREAK <td>TKTWRLIF<td>IFPIALIL<td>TLVTWTLA<td>TSVSLV<td>SYNSGAST<td>PSPLVGP<td>60</td></td></td></td></td></td></td>	TKTWRLIF <td>IFPIALIL<td>TLVTWTLA<td>TSVSLV<td>SYNSGAST<td>PSPLVGP<td>60</td></td></td></td></td></td>	IFPIALIL <td>TLVTWTLA<td>TSVSLV<td>SYNSGAST<td>PSPLVGP<td>60</td></td></td></td></td>	TLVTWTLA <td>TSVSLV<td>SYNSGAST<td>PSPLVGP<td>60</td></td></td></td>	TSVSLV <td>SYNSGAST<td>PSPLVGP<td>60</td></td></td>	SYNSGAST <td>PSPLVGP<td>60</td></td>	PSPLVGP <td>60</td>	60
QY	61	TRISRAEKIT <td>TSALG<td>SNQDVDR<td>IRYQVAL<td>LESPLAL<td>NTETT<td>IMNAIT<td>SLSYOINGA</td><td>120</td></td></td></td></td></td></td>	TSALG <td>SNQDVDR<td>IRYQVAL<td>LESPLAL<td>NTETT<td>IMNAIT<td>SLSYOINGA</td><td>120</td></td></td></td></td></td>	SNQDVDR <td>IRYQVAL<td>LESPLAL<td>NTETT<td>IMNAIT<td>SLSYOINGA</td><td>120</td></td></td></td></td>	IRYQVAL <td>LESPLAL<td>NTETT<td>IMNAIT<td>SLSYOINGA</td><td>120</td></td></td></td>	LESPLAL <td>NTETT<td>IMNAIT<td>SLSYOINGA</td><td>120</td></td></td>	NTETT <td>IMNAIT<td>SLSYOINGA</td><td>120</td></td>	IMNAIT <td>SLSYOINGA</td> <td>120</td>	SLSYOINGA	120
Dd	61	TRISRAEKIT <td>TSALG<td>SNQDVDR<td>IRYQVAL<td>LESPLAL<td>NTETT<td>IMNAIT<td>SLSYOINGA</td><td>120</td></td></td></td></td></td></td>	TSALG <td>SNQDVDR<td>IRYQVAL<td>LESPLAL<td>NTETT<td>IMNAIT<td>SLSYOINGA</td><td>120</td></td></td></td></td></td>	SNQDVDR <td>IRYQVAL<td>LESPLAL<td>NTETT<td>IMNAIT<td>SLSYOINGA</td><td>120</td></td></td></td></td>	IRYQVAL <td>LESPLAL<td>NTETT<td>IMNAIT<td>SLSYOINGA</td><td>120</td></td></td></td>	LESPLAL <td>NTETT<td>IMNAIT<td>SLSYOINGA</td><td>120</td></td></td>	NTETT <td>IMNAIT<td>SLSYOINGA</td><td>120</td></td>	IMNAIT <td>SLSYOINGA</td> <td>120</td>	SLSYOINGA	120
QY	121	SGWAPL <td>HHDDF<td>FGIGIKEL<td>IYUN<td>ASDVTS<td>FFPSAP<td>QEH<td>LNTIP<td>180</td></td></td></td></td></td></td></td>	HHDDF <td>FGIGIKEL<td>IYUN<td>ASDVTS<td>FFPSAP<td>QEH<td>LNTIP<td>180</td></td></td></td></td></td></td>	FGIGIKEL <td>IYUN<td>ASDVTS<td>FFPSAP<td>QEH<td>LNTIP<td>180</td></td></td></td></td></td>	IYUN <td>ASDVTS<td>FFPSAP<td>QEH<td>LNTIP<td>180</td></td></td></td></td>	ASDVTS <td>FFPSAP<td>QEH<td>LNTIP<td>180</td></td></td></td>	FFPSAP <td>QEH<td>LNTIP<td>180</td></td></td>	QEH <td>LNTIP<td>180</td></td>	LNTIP <td>180</td>	180
Dd	121	SGWAPL <td>HHDDF<td>FGIGIKEL<td>IYUN<td>ASDVTS<td>FFPSAP<td>QEH<td>LNTIP<td>180</td></td></td></td></td></td></td></td>	HHDDF <td>FGIGIKEL<td>IYUN<td>ASDVTS<td>FFPSAP<td>QEH<td>LNTIP<td>180</td></td></td></td></td></td></td>	FGIGIKEL <td>IYUN<td>ASDVTS<td>FFPSAP<td>QEH<td>LNTIP<td>180</td></td></td></td></td></td>	IYUN <td>ASDVTS<td>FFPSAP<td>QEH<td>LNTIP<td>180</td></td></td></td></td>	ASDVTS <td>FFPSAP<td>QEH<td>LNTIP<td>180</td></td></td></td>	FFPSAP <td>QEH<td>LNTIP<td>180</td></td></td>	QEH <td>LNTIP<td>180</td></td>	LNTIP <td>180</td>	180
QY	121	SGWAPL <td>HHDDF<td>FGIGIKEL<td>IYUN<td>ASDVTS<td>FFPSAP<td>QEH<td>LNTIP<td>180</td></td></td></td></td></td></td></td>	HHDDF <td>FGIGIKEL<td>IYUN<td>ASDVTS<td>FFPSAP<td>QEH<td>LNTIP<td>180</td></td></td></td></td></td></td>	FGIGIKEL <td>IYUN<td>ASDVTS<td>FFPSAP<td>QEH<td>LNTIP<td>180</td></td></td></td></td></td>	IYUN <td>ASDVTS<td>FFPSAP<td>QEH<td>LNTIP<td>180</td></td></td></td></td>	ASDVTS <td>FFPSAP<td>QEH<td>LNTIP<td>180</td></td></td></td>	FFPSAP <td>QEH<td>LNTIP<td>180</td></td></td>	QEH <td>LNTIP<td>180</td></td>	LNTIP <td>180</td>	180
Dd	121	SGWAPL <td>HHDDF<td>FGIGIKEL<td>IYUN<td>ASDVTS<td>FFPSAP<td>QEH<td>LNTIP<td>180</td></td></td></td></td></td></td></td>	HHDDF <td>FGIGIKEL<td>IYUN<td>ASDVTS<td>FFPSAP<td>QEH<td>LNTIP<td>180</td></td></td></td></td></td></td>	FGIGIKEL <td>IYUN<td>ASDVTS<td>FFPSAP<td>QEH<td>LNTIP<td>180</td></td></td></td></td></td>	IYUN <td>ASDVTS<td>FFPSAP<td>QEH<td>LNTIP<td>180</td></td></td></td></td>	ASDVTS <td>FFPSAP<td>QEH<td>LNTIP<td>180</td></td></td></td>	FFPSAP <td>QEH<td>LNTIP<td>180</td></td></td>	QEH <td>LNTIP<td>180</td></td>	LNTIP <td>180</td>	180
QY	181	SATVYCT <td>THNVIL<td>SGGCRD<td>SHSHQY<td>ALAGV<td>LRTA<td>GRIF<td>FEFTL<td>240</td></td></td></td></td></td></td></td>	THNVIL <td>SGGCRD<td>SHSHQY<td>ALAGV<td>LRTA<td>GRIF<td>FEFTL<td>240</td></td></td></td></td></td></td>	SGGCRD <td>SHSHQY<td>ALAGV<td>LRTA<td>GRIF<td>FEFTL<td>240</td></td></td></td></td></td>	SHSHQY <td>ALAGV<td>LRTA<td>GRIF<td>FEFTL<td>240</td></td></td></td></td>	ALAGV <td>LRTA<td>GRIF<td>FEFTL<td>240</td></td></td></td>	LRTA <td>GRIF<td>FEFTL<td>240</td></td></td>	GRIF <td>FEFTL<td>240</td></td>	FEFTL <td>240</td>	240
Dd	181	SATVYCT <td>THNVIL<td>SGGCRD<td>SHSHQY<td>ALAGV<td>LRTA<td>GRIF<td>FEFTL<td>240</td></td></td></td></td></td></td></td>	THNVIL <td>SGGCRD<td>SHSHQY<td>ALAGV<td>LRTA<td>GRIF<td>FEFTL<td>240</td></td></td></td></td></td></td>	SGGCRD <td>SHSHQY<td>ALAGV<td>LRTA<td>GRIF<td>FEFTL<td>240</td></td></td></td></td></td>	SHSHQY <td>ALAGV<td>LRTA<td>GRIF<td>FEFTL<td>240</td></td></td></td></td>	ALAGV <td>LRTA<td>GRIF<td>FEFTL<td>240</td></td></td></td>	LRTA <td>GRIF<td>FEFTL<td>240</td></td></td>	GRIF <td>FEFTL<td>240</td></td>	FEFTL <td>240</td>	240
QY	241	SATP <td>LGCDML<td>CSK<td>RYTEED<td>EDYNSA<td>VP<td>ITMA<td>HGR<td>300</td></td></td></td></td></td></td></td>	LGCDML <td>CSK<td>RYTEED<td>EDYNSA<td>VP<td>ITMA<td>HGR<td>300</td></td></td></td></td></td></td>	CSK <td>RYTEED<td>EDYNSA<td>VP<td>ITMA<td>HGR<td>300</td></td></td></td></td></td>	RYTEED <td>EDYNSA<td>VP<td>ITMA<td>HGR<td>300</td></td></td></td></td>	EDYNSA <td>VP<td>ITMA<td>HGR<td>300</td></td></td></td>	VP <td>ITMA<td>HGR<td>300</td></td></td>	ITMA <td>HGR<td>300</td></td>	HGR <td>300</td>	300
Dd	241	SATP <td>LGCDML<td>CSK<td>RYTEED<td>EDYNSA<td>VP<td>ITMA<td>HGR<td>300</td></td></td></td></td></td></td></td>	LGCDML <td>CSK<td>RYTEED<td>EDYNSA<td>VP<td>ITMA<td>HGR<td>300</td></td></td></td></td></td></td>	CSK <td>RYTEED<td>EDYNSA<td>VP<td>ITMA<td>HGR<td>300</td></td></td></td></td></td>	RYTEED <td>EDYNSA<td>VP<td>ITMA<td>HGR<td>300</td></td></td></td></td>	EDYNSA <td>VP<td>ITMA<td>HGR<td>300</td></td></td></td>	VP <td>ITMA<td>HGR<td>300</td></td></td>	ITMA <td>HGR<td>300</td></td>	HGR <td>300</td>	300
QY	301	GUGGGS	TIDR <td>WVF<td>SYVYGG<td>IKP<td>NSBED</td><td>T<td>QEGKYV<td>360</td></td></td></td></td></td>	WVF <td>SYVYGG<td>IKP<td>NSBED</td><td>T<td>QEGKYV<td>360</td></td></td></td></td>	SYVYGG <td>IKP<td>NSBED</td><td>T<td>QEGKYV<td>360</td></td></td></td>	IKP <td>NSBED</td> <td>T<td>QEGKYV<td>360</td></td></td>	NSBED	T <td>QEGKYV<td>360</td></td>	QEGKYV <td>360</td>	360
Dd	301	GUGGGS	TIDR <td>WVF<td>SYVYGG<td>IKP<td>NSBED</td><td>T<td>QEGKYV<td>360</td></td></td></td></td></td>	WVF <td>SYVYGG<td>IKP<td>NSBED</td><td>T<td>QEGKYV<td>360</td></td></td></td></td>	SYVYGG <td>IKP<td>NSBED</td><td>T<td>QEGKYV<td>360</td></td></td></td>	IKP <td>NSBED</td> <td>T<td>QEGKYV<td>360</td></td></td>	NSBED	T <td>QEGKYV<td>360</td></td>	QEGKYV <td>360</td>	360
QY	361	PGAF <td>GGKRIQ<td>ALIL<td>IKV<td>STSL<td>GED</td><td>VL<td>TVPP<td>420</td></td></td></td></td></td></td>	GGKRIQ <td>ALIL<td>IKV<td>STSL<td>GED</td><td>VL<td>TVPP<td>420</td></td></td></td></td></td>	ALIL <td>IKV<td>STSL<td>GED</td><td>VL<td>TVPP<td>420</td></td></td></td></td>	IKV <td>STSL<td>GED</td><td>VL<td>TVPP<td>420</td></td></td></td>	STSL <td>GED</td> <td>VL<td>TVPP<td>420</td></td></td>	GED	VL <td>TVPP<td>420</td></td>	TVPP <td>420</td>	420
Dd	361	PGAF <td>GGKRIQ<td>ALIL<td>IKV<td>STSL<td>GED</td><td>VL<td>TVPP<td>420</td></td></td></td></td></td></td>	GGKRIQ <td>ALIL<td>IKV<td>STSL<td>GED</td><td>VL<td>TVPP<td>420</td></td></td></td></td></td>	ALIL <td>IKV<td>STSL<td>GED</td><td>VL<td>TVPP<td>420</td></td></td></td></td>	IKV <td>STSL<td>GED</td><td>VL<td>TVPP<td>420</td></td></td></td>	STSL <td>GED</td> <td>VL<td>TVPP<td>420</td></td></td>	GED	VL <td>TVPP<td>420</td></td>	TVPP <td>420</td>	420
QY	421	FSPAL <td>LYP<td>MTV<td>SNK<td>TATL<td>HS<td>PT<td>ENAF<td>480</td></td></td></td></td></td></td></td>	LYP <td>MTV<td>SNK<td>TATL<td>HS<td>PT<td>ENAF<td>480</td></td></td></td></td></td></td>	MTV <td>SNK<td>TATL<td>HS<td>PT<td>ENAF<td>480</td></td></td></td></td></td>	SNK <td>TATL<td>HS<td>PT<td>ENAF<td>480</td></td></td></td></td>	TATL <td>HS<td>PT<td>ENAF<td>480</td></td></td></td>	HS <td>PT<td>ENAF<td>480</td></td></td>	PT <td>ENAF<td>480</td></td>	ENAF <td>480</td>	480
Dd	421	FSPAL <td>LYP<td>MTV<td>SNK<td>TATL<td>HS<td>PT<td>ENAF<td>480</td></td></td></td></td></td></td></td>	LYP <td>MTV<td>SNK<td>TATL<td>HS<td>PT<td>ENAF<td>480</td></td></td></td></td></td></td>	MTV <td>SNK<td>TATL<td>HS<td>PT<td>ENAF<td>480</td></td></td></td></td></td>	SNK <td>TATL<td>HS<td>PT<td>ENAF<td>480</td></td></td></td></td>	TATL <td>HS<td>PT<td>ENAF<td>480</td></td></td></td>	HS <td>PT<td>ENAF<td>480</td></td></td>	PT <td>ENAF<td>480</td></td>	ENAF <td>480</td>	480
QY	481	NHTLR <td>GF<td>FG</td><td>MTL<td>DSQ</td><td>AR<td>LN<td>PSA</td><td>540</td></td></td></td></td>	GF <td>FG</td> <td>MTL<td>DSQ</td><td>AR<td>LN<td>PSA</td><td>540</td></td></td></td>	FG	MTL <td>DSQ</td> <td>AR<td>LN<td>PSA</td><td>540</td></td></td>	DSQ	AR <td>LN<td>PSA</td><td>540</td></td>	LN <td>PSA</td> <td>540</td>	PSA	540
Dd	481	NHTLR <td>GF<td>FG</td><td>MTL<td>DSQ</td><td>AR</td><td>LN<td>PSA</td><td>540</td></td></td></td>	GF <td>FG</td> <td>MTL<td>DSQ</td><td>AR</td><td>LN<td>PSA</td><td>540</td></td></td>	FG	MTL <td>DSQ</td> <td>AR</td> <td>LN<td>PSA</td><td>540</td></td>	DSQ	AR	LN <td>PSA</td> <td>540</td>	PSA	540
QY	541	YCL <td>SL<td>AE<td>IS</td><td>NTL<td>FG</td><td>FR<td>IV<td>577</td></td></td></td></td></td>	SL <td>AE<td>IS</td><td>NTL<td>FG</td><td>FR<td>IV<td>577</td></td></td></td></td>	AE <td>IS</td> <td>NTL<td>FG</td><td>FR<td>IV<td>577</td></td></td></td>	IS	NTL <td>FG</td> <td>FR<td>IV<td>577</td></td></td>	FG	FR <td>IV<td>577</td></td>	IV <td>577</td>	577
Dd	541	YCL <td>SL<td>AE</td><td>IS</td><td>NTL<td>FG</td><td>FR<td>IV<td>577</td></td></td></td></td>	SL <td>AE</td> <td>IS</td> <td>NTL<td>FG</td><td>FR<td>IV<td>577</td></td></td></td>	AE	IS	NTL <td>FG</td> <td>FR<td>IV<td>577</td></td></td>	FG	FR <td>IV<td>577</td></td>	IV <td>577</td>	577

RESULT 4

090340 PRELIMINARY; PRT: 577 AA.

AC 090340; PRT: 577 AA.

DT 01-NOV-1998 (TEMBLrel. 08, Created)

DT 01-NOV-1998 (TEMBLrel. 08, Last sequence update)

DT 01-JUN-2001 (TEMBLrel. 17, last annotation update)

DE Hemagglutinin-neuraminidase.

GN HN.

OS Newcastle disease virus.

OC Viruses; ssRNA negative-strand viruses; Mononegavirales;

OC Paramyxoviridae; Paramyxovirinae; Rubulaviruses.

NCBI TaxID=111176;

RN NCBI [1]

RN SEQUENCE FROM N.A.

RN STRAIN=LASOTA;

RN RC de Leeuw O.S.; Peeters B.P.H.;

RA "Complete nucleotide sequence of Newcastle disease virus: evidence for

RT the existence of a new gene within the subfamily Paramyxovirinae.";

RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.

RN [2]

RA SEQUENCE FROM N.A.

RP Roemer-Overdorfer A.; Buchholz U.J.; Mundt E.; Mettenleiter T.C.;

RT "Generation of recombinant lentogenic Newcastle Disease Virus from

RL cDNA.";

RN Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.

RN [3]

RA SEQUENCE FROM N.A.

RP Roemer-Overdorfer A.;

RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.

RE EMBL; AF077761; AAC28376.1; -.

DR	EMBL: Y18898; CAB51326.1; -	DR	InterPro: IPR000665; Hem-neuramndse.
DR	Pfam: PF00423; HN; 1.	DR	Pfam: PF00423; HN; 1.
DR	SEQUENCE 577 AA; 63213 MW; 66D63PA1B3041EB4 CRC64;	DR	SEQUENCE 577 AA; 63213 MW; 66D63PA1B3041EB4 CRC64;
DR	EMBL: Y18898; CAB51326.1; -	DR	InterPro: IPR000665; Hem-neuramndse.
DR	Pfam: PF00423; HN; 1.	DR	Pfam: PF00423; HN; 1.
DR	SEQUENCE 577 AA; 63213 MW; 66D63PA1B3041EB4 CRC64;	DR	SEQUENCE 577 AA; 63213 MW; 66D63PA1B3041EB4 CRC64;
DR	Query Match	DR	Query Match
DR	Best Local Similarity 97.4%; Score 2920; DB 12; Length 577;	DR	Best Local Similarity 97.1%; Pred. No. 4.9e-231;
DR	Matches 560; Conservative 8; Mismatches 9; Indels 0; Gaps 0;	DR	Matches 560; Conservative 8; Mismatches 9; Indels 0; Gaps 0;
DR	1 MDRASGVALLENDERAKNTWRLIFRIALLTLVVTATSVASLVVSGASTPDLVGP 60	DR	1 MDRASGVALLENDERAKNTWRLIFRIALLTLVVTATSVASLVVSGASTPDLVGP 60
DR	1 MDRASGVALLENDERAKNTWRLIFRIALLTLVVTATSVASLVVSGASTPDLVGP 60	DR	1 MDRASGVALLENDERAKNTWRLIFRIALLTLVVTATSVASLVVSGASTPDLVGP 60
DR	61 TRIRAEKITSALGSNOVDYDRLYKQVAALESPALLANTETTINNAITSYQINGAAN 120	DR	61 TRIRAEKITSALGSNOVDYDRLYKQVAALESPALLANTETTINNAITSYQINGAAN 120
DR	61 TRIRAEKITSALGSNOVDYDRLYKQVAALESPALLANTETTINNAITSYQINGAAN 120	DR	61 TRIRAEKITSALGSNOVDYDRLYKQVAALESPALLANTETTINNAITSYQINGAAN 120
DR	121 SGWAPFHPDPFGIGIGIKELIVDASVTSYPSPAFQEHNFIPAPPTGSGCRRIPSPDM 180	DR	121 SGWAPFHPDPFGIGIGIKELIVDASVTSYPSPAFQEHNFIPAPPTGSGCRRIPSPDM 180
DR	121 SGWAPFHPDPFGIGIGIKELIVDASVTSYPSPAFQEHNFIPAPPTGSGCRRIPSPDM 180	DR	121 SGWAPFHPDPFGIGIGIKELIVDASVTSYPSPAFQEHNFIPAPPTGSGCRRIPSPDM 180
DR	181 SATHYCVTHNVILSGCRDHSQHYTALGVLRATATARRIFPSTLRSISLDDTONRKSCSV 240	DR	181 SATHYCVTHNVILSGCRDHSQHYTALGVLRATATARRIFPSTLRSISLDDTONRKSCSV 240
DR	181 SATHYCVTHNVILSGCRDHSQHYTALGVLRATATARRIFPSTLRSISLDDTONRKSCSV 240	DR	181 SATHYCVTHNVILSGCRDHSQHYTALGVLRATATARRIFPSTLRSISLDDTONRKSCSV 240
DR	241 SATPLGCDMLCSKTLTEFEEDDYNASVPTTLMAHGLGPDQYHEKOLDVYTLFEDWVANP 300	DR	241 SATPLGCDMLCSKTLTEFEEDDYNASVPTTLMAHGLGPDQYHEKOLDVYTLFEDWVANP 300
DR	241 SATPLGCDMLCSKTLTEFEEDDYNASVPTTLMAHGLGPDQYHEKOLDVYTLFEDWVANP 300	DR	241 SATPLGCDMLCSKTLTEFEEDDYNASVPTTLMAHGLGPDQYHEKOLDVYTLFEDWVANP 300
DR	301 GVGGGSPFDGRVWVSYYGGAKPNPSPSTVQEGKVIYKRVNDTCPEBDYQOIRAKSSYK 360	DR	301 GVGGGSPFDGRVWVSYYGGAKPNPSPSTVQEGKVIYKRVNDTCPEBDYQOIRAKSSYK 360
DR	301 GVGGGSPFDGRVWVSYYGGAKPNPSPSTVQEGKVIYKRVNDTCPEBDYQOIRAKSSYK 360	DR	301 GVGGGSPFDGRVWVSYYGGAKPNPSPSTVQEGKVIYKRVNDTCPEBDYQOIRAKSSYK 360
DR	361 PGRFGGRIRIQOALISIKVSTSLGEPPLVTPPNTVTLMAEGRIILVGTSHFLYQRSSY 420	DR	361 PGRFGGRIRIQOALISIKVSTSLGEPPLVTPPNTVTLMAEGRIILVGTSHFLYQRSSY 420
DR	361 PGRFGGRIRIQOALISIKVSTSLGEPPLVTPPNTVTLMAEGRIILVGTSHFLYQRSSY 420	DR	361 PGRFGGRIRIQOALISIKVSTSLGEPPLVTPPNTVTLMAEGRIILVGTSHFLYQRSSY 420
DR	421 FSPALLVPMVSNKTATILHSPYFNATFRPGSIPQOASAPCPNSCVTVYTDPPYLLFYR 480	DR	421 FSPALLVPMVSNKTATILHSPYFNATFRPGSIPQOASAPCPNSCVTVYTDPPYLLFYR 480
DR	421 FSPALLVPMVSNKTATILHSPYFNATFRPGSIPQOASAPCPNSCVTVYTDPPYLLFYR 480	DR	421 FSPALLVPMVSNKTATILHSPYFNATFRPGSIPQOASAPCPNSCVTVYTDPPYLLFYR 480
DR	481 NHTLRGFGTMDSEQARLNPAASVPEPSTSRSRTRVSSSSTKAAVYTSICFKVVKTKNT 540	DR	481 NHTLRGFGTMDSEQARLNPAASVPEPSTSRSRTRVSSSSTKAAVYTSICFKVVKTKNT 540
DR	481 NHTLRGFGTMDSEQARLNPAASVPEPSTSRSRTRVSSSSTKAAVYTSICFKVVKTKNT 540	DR	481 NHTLRGFGTMDSEQARLNPAASVPEPSTSRSRTRVSSSSTKAAVYTSICFKVVKTKNT 540
DR	541 YCLSIATISNTLFGFPRIVPLVAILNDQVREARSG 577	DR	541 YCLSIATISNTLFGFPRIVPLVAILNDQVREARSG 577
DR	541 YCLSIATISNTLFGFPRIVPLVAILNDQVREARSG 577	DR	541 YCLSIATISNTLFGFPRIVPLVAILNDQVREARSG 577
DR	SEQUENCE 577 AA; 63227 MW; 23D667483520C8C17 CRC64;	DR	SEQUENCE 577 AA; 63227 MW; 23D667483520C8C17 CRC64;

Query Match 97.3%; Score 2917; DB 12; Length 577;  
Best Local Similarity 96.9%; Pred. No. 8, 7e-231;  
Matches 559; Conservative 8; Mismatches 10; Indels 0; Gaps 0;

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QY 1 MDRVAVQVLENDEREAKNTWRLIFRIAILLLTVVTLLATSVASLYVSMGASTPSDLVGP 60
DB 1 MDRVAVQVLENDEREAKNTWRLIFRIAILLLTVVTLLATSVASLYVSMGASTPSDLVGP 60
QY 61 TRISRAEEKITSLGSDNODVDRIRYQVAVLESPALLNTEITIMNATISLSYQINGANN 120
DB 61 TRISRAEEKITSLGSDNODVDRIRYQVAVLESPALLNTEITIMNATISLSYQINGANN 120
QY 121 SGCGAPIHDPDYGIGIKELIVDNASDVTSFYPSPAFQEHNFIPAPPTGSGCTRIIPSDM 180
DB 121 SGCGAPIHDPDYGIGIKELIVDNASDVTSFYPSPAFQEHNFIPAPPTGSGCTRIIPSDM 180
QY 181 SATHYCYTHNVILSGCRDHS HQYLALGVLTATGRIFSTLSISLDDTONRKSCSV 240
DB 181 SATHYCYTHNVILSGCRDHS HQYLALGVLTATGRIFSTLSISLDDTONRKSCSV 240
QY 241 SATPLGCDMLCSKATETEEDYNSAVPTLMAHGRIGFDQYHEKDLDTTLFGDWVANY 300
DB 241 SATPLGCDMLCSKATETEEDYNSAVPTLMAHGRIGFDQYHEKDLDTTLFGDWVANY 300
QY 301 GVGGSFIDGRVWFSYVGLKPNSPDVTQEGKYIYKRYNDCPEEDQYQIRMAKSSYK 360
DB 301 GVGGSFIDGRVWFSYVGLKPNSPDVTQEGKYIYKRYNDCPEEDQYQIRMAKSSYK 360
QY 361 GVGGSFIDGRVWFSYVGLKPNSPDVTQEGKYIYKRYNDCPEEDQYQIRMAKSSYK 360
DB 361 GVGGSFIDGRVWFSYVGLKPNSPDVTQEGKYIYKRYNDCPEEDQYQIRMAKSSYK 360
QY 421 FSPALLYPMVTSNKTATLHSPYTFNAFTPGSIPCOASARCNSCVGYVTDPPYLIFR 480
DB 421 FSPALLYPMVTSNKTATLHSPYTFNAFTPGSIPCOASARCNSCVGYVTDPPYLIFR 480
QY 481 NHTLRGVFGTMDSEQARLNPAASVFDSTSRIRTRVSSSTKAAVYTSCTCKVKTNTK 540
DB 481 NHTLRGVFGTMDSEQARLNPAASVFDSTSRIRTRVSSSTKAAVYTSCTCKVKTNTK 540
QY 541 YCLISAEISNTLFGFRIPLVLEILKNDGVREARSG 577
DB 541 YCLISAEISNTLFGFRIPLVLEILKNDGVREARSG 577
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## RESULT 6

Q91AH7 PRELIMINARY; PRT; 577 AA.

AC Q91AH7; PRELIMINARY; PRT; 577 AA.  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)  
DE Hemagglutinin-neuraminidase.  
GN HN.  
OS Newcastle disease virus.  
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;  
OC Paramyxoviridae; Paramyxovirinae; Rubulaviruses.  
OC NCBI\_TaxID=11176;  
OX NCBI\_TaxID=11176;  
RP SEQUENCE FROM N.A.  
RC STRAIN=B1;  
RX MEDLINE=21548317; PubMed=11689668;  
RA Nakaya T., Cros J., Park M.S., Nakaya Y., Zheng H., Sagstera A.,  
Villar E., Garcia-Sastre A., Palese P.;  
RT "Recombinant Newcastle disease virus as a vaccine vector.";  
RT J. Virol. 75:11868-11873(2001).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=B1;  
RA Nakaya T., Garcia-Sastre A., Palese P.;  
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF375823; AAK55551.1; -.

DR InterPro; IPR000665; Hem-neuramndae.  
DR Pfam; PF00423; HN; 1.  
SQ SEQUENCE 577 AA; 63216 MW; D5A26F305A885969 CRC64;

Query Match 97.2%; Score 2915; DB 12; Length 577;  
Best Local Similarity 96.7%; Pred. No. 1.3e-230;  
Matches 558; Conservative 9; Mismatches 10; Indels 0; Gaps 0;

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QY 1 MDRVAVQVLENDEREAKNTWRLIFRIAILLLTVVTLLATSVASLYVSMGASTPSDLVGP 60
DB 1 MDRVAVQVLENDEREAKNTWRLIFRIAILLLTVVTLLATSVASLYVSMGASTPSDLVGP 60
QY 61 TRISRAEEKITSLGSDNODVDRIRYQVAVLESPALLNTEITIMNATISLSYQINGANN 120
DB 61 TRISRAEEKITSLGSDNODVDRIRYQVAVLESPALLNTEITIMNATISLSYQINGANN 120
QY 121 SGCGAPIHDPDYGIGIKELIVDNASDVTSFYPSPAFQEHNFIPAPPTGSGCTRIIPSDM 180
DB 121 SGCGAPIHDPDYGIGIKELIVDNASDVTSFYPSPAFQEHNFIPAPPTGSGCTRIIPSDM 180
QY 181 SATHYCYTHNVILSGCRDHS HQYLALGVLTATGRIFSTLSISLDDTONRKSCSV 240
DB 181 SATHYCYTHNVILSGCRDHS HQYLALGVLTATGRIFSTLSISLDDTONRKSCSV 240
QY 241 SATPLGCDMLCSKATETEEDYNSAVPTLMAHGRIGFDQYHEKDLDTTLFGDWVANY 300
DB 241 SATPLGCDMLCSKATETEEDYNSAVPTLMAHGRIGFDQYHEKDLDTTLFGDWVANY 300
QY 301 GVGGSFIDGRVWFSYVGLKPNSPDVTQEGKYIYKRYNDCPEEDQYQIRMAKSSYK 360
DB 301 GVGGSFIDGRVWFSYVGLKPNSPDVTQEGKYIYKRYNDCPEEDQYQIRMAKSSYK 360
QY 361 GVGGSFIDGRVWFSYVGLKPNSPDVTQEGKYIYKRYNDCPEEDQYQIRMAKSSYK 360
DB 361 GVGGSFIDGRVWFSYVGLKPNSPDVTQEGKYIYKRYNDCPEEDQYQIRMAKSSYK 360
QY 421 FSPALLYPMVTSNKTATLHSPYTFNAFTPGSIPCOASARCNSCVGYVTDPPYLIFR 480
DB 421 FSPALLYPMVTSNKTATLHSPYTFNAFTPGSIPCOASARCNSCVGYVTDPPYLIFR 480
QY 481 NHTLRGVFGTMDSEQARLNPAASVFDSTSRIRTRVSSSTKAAVYTSCTCKVKTNTK 540
DB 481 NHTLRGVFGTMDSEQARLNPAASVFDSTSRIRTRVSSSTKAAVYTSCTCKVKTNTK 540
QY 541 YCLISAEISNTLFGFRIPLVLEILKNDGVREARSG 577
DB 541 YCLISAEISNTLFGFRIPLVLEILKNDGVREARSG 577
```

## RESULT 7

Q8B9S0 PRELIMINARY; PRT; 577 AA.

AC Q8B9S0; PRELIMINARY; PRT; 577 AA.  
DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
DE Hemagglutinin-neuraminidase protein HN.  
OS Newcastle disease virus.  
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;  
OC Paramyxoviridae; Paramyxovirinae; Rubulaviruses.  
OC NCBI\_TaxID=11176;  
OX NCBI\_TaxID=11176;  
RP SEQUENCE FROM N.A.  
RC STRAIN=MET95;  
RA Murakawa Y., Sakaguchi M., Soejima K., Eriuchi S., Takase K.,  
Sueyoshi M., Nagatomo H., Ito T., Otsuki K.;  
RT "Haemagglutinating activity of the lentogenic Newcastle disease virus  
strain MET95.";  
RT Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY143159; AA018268.1; -.  
SQ SEQUENCE 577 AA; 63269 MW; 1B3EA99008B5AF42 CRC64;

Query Match 97.2%; Score 2915; DB 12; Length 577;

Best Local Similarity 96.5%; Pred. No. 1.3e-230;  
Matches 557; Conservative 10; Mismatches 10; Indels 0; Gaps 0;

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QY 1 MDRASQVLENDEREAKNTWRLIFRIAILLTAVTLATSVASLVSGASTPSDLVGP 60
Db 1 MDRASQVLENDEREAKNTWRLIFRIAILLTAVTLATSVASLVSGASTPSDLVGP 60
QY 61 TRISRAEKTITSGNODVVDRIYKQVLESPLALNTETTINMATSLSYQINGAAN 120
Db 61 TRISRAEKTITSGNODVVDRIYKQVLESPLALNTETTINMATSLSYQINGAAN 120
QY 121 SGWAPLHDPDPIGIGIKELIVDNASDVTSPYPAFOEHLNFIAPPTGSGCTRI 180
Db 121 SGWAPLHDPDPIGIGIKELIVDNASDVTSPYPAFOEHLNFIAPPTGSGCTRI 180
QY 121 SGWAPLHDPDPIGIGIKELIVDNASDVTSPYPAFOEHLNFIAPPTGSGCTRI 180
Db 121 SGWAPLHDPDPIGIGIKELIVDNASDVTSPYPAFOEHLNFIAPPTGSGCTRI 180
QY 181 SATHYCTHNVILSGCRDHSYHOLAGVLRRTATGRIFPSTLRSLDTONRKSCSV 240
Db 181 SATHYCTHNVILSGCRDHSYHOLAGVLRRTATGRIFPSTLRSLDTONRKSCSV 240
QY 241 SATPLGCDMLCSKYTEEEDYNSAVPTLMAHGRIGDQYHEKDLVTTLFEDMVANYP 300
Db 241 SATPLGCDMLCSKYTEEEDYNSAVPTLMAHGRIGDQYHEKDLVTTLFEDMVANYP 300
QY 241 SATPLGCDMLCSKYTEEEDYNSAVPTLMAHGRIGDQYHEKDLVTTLFEDMVANYP 300
Db 241 SATPLGCDMLCSKYTEEEDYNSAVPTLMAHGRIGDQYHEKDLVTTLFEDMVANYP 300
QY 301 GVGGSSTIDGRWVSVYGGKLPNSPDTVOEGKYIYKRYNDTCPEODYQIRMAKSSYK 360
Db 301 GVGGSSTIDGRWVSVYGGKLPNSPDTVOEGKYIYKRYNDTCPEODYQIRMAKSSYK 360
QY 301 GVGGSSTIDGRWVSVYGGKLPNSPDTVOEGKYIYKRYNDTCPEODYQIRMAKSSYK 360
Db 301 GVGGSSTIDGRWVSVYGGKLPNSPDTVOEGKYIYKRYNDTCPEODYQIRMAKSSYK 360
QY 361 PGRFGKRIQOAILISIKVSTSLGEPVLTPPNTVTLMGAGRLITVGTSHFLYQSGSSY 420
Db 361 PGRFGKRIQOAILISIKVSTSLGEPVLTPPNTVTLMGAGRLITVGTSHFLYQSGSSY 420
QY 421 FSPALLVPMVSNKTATLHSPYTENAFTRPQASARCPNSCVTVYDPIPLFYR 480
Db 421 FSPALLVPMVSNKTATLHSPYTENAFTRPQASARCPNSCVTVYDPIPLFYR 480
QY 421 FSPALLVPMVSNKTATLHSPYTENAFTRPQASARCPNSCVTVYDPIPLFYR 480
Db 421 FSPALLVPMVSNKTATLHSPYTENAFTRPQASARCPNSCVTVYDPIPLFYR 480
QY 481 NHTLRGVFGTMDSEQARLPASAVFSDTSRSRITRVSSSTKAAYTSTCFKVKTKNT 540
Db 481 NHTLRGVFGTMDSEQARLPASAVFSDTSRSRITRVSSSTKAAYTSTCFKVKTKNT 540
QY 541 YCISIAEISNTLFGEPRIPLVLEILKDDGVREARSG 577
Db 541 YCISIAEISNTLFGEPRIPLVLEILKDDGVREARSG 577
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## RESULT 8

083842 PRELIMINARY; PRT; 577 AA.

AC 083842; DT 01-NOV-1996 (TREMBlrel. 01, Created)  
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)  
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)  
DE Hemagglutinin-neuraminidase.  
OS Newcastle disease virus.  
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;  
OC Paramyxoviridae; Paramyxovirinae; Rubulavirus.  
CX NCBI\_TaxID=11176;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Vaccine 1;  
RX MEDLINE=96414821; PubMed=8817822;  
RA Seal B.S., King D.J., Bennett J.D.;  
RT "Characterization of Newcastle disease virus vaccines by biological  
RT properties and sequence analysis of the hemagglutinin-neuraminidase  
RT protein gene.";  
RL Vaccine 14:761-766 (1996).  
DR EMBL; U37187; AAC55041.1; -;  
DR InterPro; IPR000665; Hem-neuramndse.  
DR Pfam; PF00423; HN; 1.  
SQ SEQUENCE 577 AA; 63213 MM; 59DE7068352C8C16 CRC64;

Query Match 97.2%; Score 2913; DB 12; Length 577;  
Best Local Similarity 96.7%; Pred. No. 1.9e-230;  
Matches 558; Conservative 8; Mismatches 11; Indels 0; Gaps 0;

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QY 1 MDRASQVLENDEREAKNTWRLIFRIAILLTAVTLATSVASLVSGASTPSDLVGP 60
Db 1 MDRASQVLENDEREAKNTWRLIFRIAILLTAVTLATSVASLVSGASTPSDLVGP 60
QY 61 TRISRAEKTITSGNODVVDRIYKQVLESPLALNTETTINMATSLSYQINGAAN 120
Db 61 TRISRAEKTITSGNODVVDRIYKQVLESPLALNTETTINMATSLSYQINGAAN 120
QY 121 SGWAPLHDPDPIGIGIKELIVDNASDVTSPYPAFOEHLNFIAPPTGSGCTRI 180
Db 121 SGWAPLHDPDPIGIGIKELIVDNASDVTSPYPAFOEHLNFIAPPTGSGCTRI 180
QY 121 SGWAPLHDPDPIGIGIKELIVDNASDVTSPYPAFOEHLNFIAPPTGSGCTRI 180
Db 121 SGWAPLHDPDPIGIGIKELIVDNASDVTSPYPAFOEHLNFIAPPTGSGCTRI 180
QY 181 SATHYCTHNVILSGCRDHSYHOLAGVLRRTATGRIFPSTLRSLDTONRKSCSV 240
Db 181 SATHYCTHNVILSGCRDHSYHOLAGVLRRTATGRIFPSTLRSLDTONRKSCSV 240
QY 241 SATPLGCDMLCSKYTEEEDYNSAVPTLMAHGRIGDQYHEKDLVTTLFEDMVANYP 300
Db 241 SATPLGCDMLCSKYTEEEDYNSAVPTLMAHGRIGDQYHEKDLVTTLFEDMVANYP 300
QY 241 SATPLGCDMLCSKYTEEEDYNSAVPTLMAHGRIGDQYHEKDLVTTLFEDMVANYP 300
Db 241 SATPLGCDMLCSKYTEEEDYNSAVPTLMAHGRIGDQYHEKDLVTTLFEDMVANYP 300
QY 301 GVGGSSTIDGRWVSVYGGKLPNSPDTVOEGKYIYKRYNDTCPEODYQIRMAKSSYK 360
Db 301 GVGGSSTIDGRWVSVYGGKLPNSPDTVOEGKYIYKRYNDTCPEODYQIRMAKSSYK 360
QY 301 GVGGSSTIDGRWVSVYGGKLPNSPDTVOEGKYIYKRYNDTCPEODYQIRMAKSSYK 360
Db 301 GVGGSSTIDGRWVSVYGGKLPNSPDTVOEGKYIYKRYNDTCPEODYQIRMAKSSYK 360
QY 361 PGRFGKRIQOAILISIKVSTSLGEPVLTPPNTVTLMGAGRLITVGTSHFLYQSGSSY 420
Db 361 PGRFGKRIQOAILISIKVSTSLGEPVLTPPNTVTLMGAGRLITVGTSHFLYQSGSSY 420
QY 421 FSPALLVPMVSNKTATLHSPYTENAFTRPQASARCPNSCVTVYDPIPLFYR 480
Db 421 FSPALLVPMVSNKTATLHSPYTENAFTRPQASARCPNSCVTVYDPIPLFYR 480
QY 421 FSPALLVPMVSNKTATLHSPYTENAFTRPQASARCPNSCVTVYDPIPLFYR 480
Db 421 FSPALLVPMVSNKTATLHSPYTENAFTRPQASARCPNSCVTVYDPIPLFYR 480
QY 481 NHTLRGVFGTMDSEQARLPASAVFSDTSRSRITRVSSSTKAAYTSTCFKVKTKNT 540
Db 481 NHTLRGVFGTMDSEQARLPASAVFSDTSRSRITRVSSSTKAAYTSTCFKVKTKNT 540
QY 541 YCISIAEISNTLFGEPRIPLVLEILKDDGVREARSG 577
Db 541 YCISIAEISNTLFGEPRIPLVLEILKDDGVREARSG 577
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## RESULT 9

09W9H0 PRELIMINARY; PRT; 577 AA.

AC 09W9H0; DT 01-NOV-1999 (TREMBlrel. 12, Created)  
DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)  
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)  
DE Hemagglutinin-neuraminidase.  
CN HN.  
OS Newcastle disease virus.  
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;  
OC Paramyxoviridae; Paramyxovirinae; Rubulavirus.  
CX NCBI\_TaxID=11176;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=SAH/85;  
RA Grishanov O.G., Starov S.K., Lomakin A.I., Smolensky V.I., Drygin V.V.,  
RA Grishanov O.G., Starov S.K., Lomakin A.I., Smolensky V.I., Drygin V.V.,  
RA Grishanov O.G., Starov S.K., Lomakin A.I., Smolensky V.I., Drygin V.V.,  
RA Grishanov O.G., Starov S.K., Lomakin A.I., Smolensky V.I., Drygin V.V.,  
RT "Phylogenetic analysis of Newcastle disease virus of Russia.";  
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=SAH/85;  
RA Grishanov O.G., Starov S.K., Lomakin A.I., Smolensky V.I., Drygin V.V.,  
RA Grishanov O.G., Starov S.K., Lomakin A.I., Smolensky V.I., Drygin V.V.,  
RA Grishanov O.G., Starov S.K., Lomakin A.I., Smolensky V.I., Drygin V.V.,  
RA Grishanov O.G., Starov S.K., Lomakin A.I., Smolensky V.I., Drygin V.V.,  
RT "Phylogenetic analysis of Newcastle disease virus of Russia.";  
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL; Y19021; CAB50912.1; -;  
DR EMBL; AJ243384; CAB46065.1; -;  
DR InterPro; IPR000665; Hem-neuramndse.  
DR Pfam; PF00423; HN; 1.

SQL SEQUENCE 577 AA; 63181 MW; E2C045E98FEBAAA CRC64;  
Query Match 96.8%; Score 2902; DB 12; Length 577;  
Best Local Similarity 96.4%; Pred. No. 1.5e-229;  
Matches 556; Conservative 11; Mismatches 10; Indels 0; Gaps 0;  
QY 1 MDRASQVLENDERBAKNTWRLIFRIAILLTVVTLATSVASLVYSGASTPSDLVGP 60  
DB 1 MDRASQVLENDERBAKNTWRLIFRIAILLTVVTLATSVASLVYSGASTPSDLVGP 60  
QY 61 TRISRAEEKTALSAGSNQDVVDRIYKQVLESPLALINTEITMAITSLSYINGAANN 120  
DB 61 TRISRAEEKTALSAGSNQDVVDRIYKQVLESPLALINTEITMAITSLSYINGAANN 120  
QY 61 TRISRAEEKTALSAGSNQDVVDRIYKQVLESPLALINTEITMAITSLSYINGAANN 120  
DB 61 TRISRAEEKTALSAGSNQDVVDRIYKQVLESPLALINTEITMAITSLSYINGAANN 120  
QY 121 SCMGAPLHDDPFIIGIGKELIVNADSVTSFYPSAQOEHLNFIIPATTSGCCRIIPSPDM 180  
DB 121 SCMGAPLHDDPFIIGIGKELIVNADSVTSFYPSAQOEHLNFIIPATTSGCCRIIPSPDM 180  
QY 181 SATHYCYTNHVLISGCRDHS HQYLALGVLTATGRIFFSTLRSISLDDTONRKSCSV 240  
DB 181 SATHYCYTNHVLISGCRDHS HQYLALGVLTATGRIFFSTLRSISLDDTONRKSCSV 240  
QY 241 SATPLGCDMLCSKYTEEBEDYNSAVPTMAHGRIGFDQYHEKLDVTTLPEDWYANP 300  
DB 241 SATPLGCDMLCSKYTEEBEDYNSAVPTMAHGRIGFDQYHEKLDVTTLPEDWYANP 300  
QY 301 GVGGSFIDGRVWFVSYYGGLKPNSSPDTVOEGKYIYKRYNDTCPEBODYQIRMAKSSYK 360  
DB 301 GVGGSFIDGRVWFVSYYGGLKPNSSPDTVOEGKYIYKRYNDTCPEBODYQIRMAKSSYK 360  
QY 361 PGRFGKRIQOAILSIKYSTSLGEBPVLTPPNTVTLMAEGRILTVGTSHPLYORGSY 420  
DB 361 PGRFGKRIQOAILSIKYSTSLGEBPVLTPPNTVTLMAEGRILTVGTSHPLYORGSY 420  
QY 421 FSPALLPYMTVSNKATLHSPYTFNAPTRPGSIPOCASARCPNSCTGYTDPYPLIFR 480  
DB 421 FSPALLPYMTVSNKATLHSPYTFNAPTRPGSIPOCASARCPNSCTGYTDPYPLIFR 480  
QY 481 NHTLRGVFGTMDSEQARLNPAASVPDSTRSRITRVSSTRAAYTSTCFKVVTKNTK 540  
DB 481 NHTLRGVFGTMDSEQARLNPAASVPDSTRSRITRVSSTRAAYTSTCFKVVTKNTK 540  
QY 541 YCLSTIAEISNTLFGERRIYPLVEILKNDGVREARSG 577  
DB 541 YCLSTIAEISNTLFGERRIYPLVEILKNDGVREARSG 577  
RESULT 10  
Q8BA53 PRELIMINARY; PRT; 577 AA.  
AC Q8BA53;  
DT 01-MAR-2003 (TREMBLrel. 23, Created)  
DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)  
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)  
DE Hemagglutinin-neuraminidase.  
OS Newcastle disease virus.  
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;  
OC Paramyxoviridae; Paramyxovirinae; Rubulaviruses;  
OC NCBI\_TaxID=11176;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=23/2000;  
RA Zhou J.Y., Ye J.X., Chen Q.X., Wang J.Y., Chen J.G., Cheng L.Q.;  
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY135171; AAN08047.1; -  
SQ SEQUENCE 577 AA; 63236 MW; 5EBCLA979387AB3A CRC64;  
Query Match 96.6%; Score 2897; DB 12; Length 577;  
Best Local Similarity 96.4%; Pred. No. 3.8e-229;  
Matches 556; Conservative 9; Mismatches 12; Indels 0; Gaps 0;  
QY 1 MDRASQVLENDERBAKNTWRLIFRIAILLTVVTLATSVASLVYSGASTPSDLVGP 60  
DB 1 MDRASQVLENDERBAKNTWRLIFRIAILLTVVTLATSVASLVYSGASTPSDLVGP 60

DB 1 MDRASQVLENDERBAKNTWRLIFRIAILLTVVTLATSVASLVYSGASTPSDLVGP 60  
QY 61 TRISRAEEKTALSAGSNQDVVDRIYKQVLESPLALINTEITMAITSLSYINGAANN 120  
DB 61 TRISRAEEKTALSAGSNQDVVDRIYKQVLESPLALINTEITMAITSLSYINGAANN 120  
QY 121 SCMGAPLHDDPFIIGIGKELIVNADSVTSFYPSAQOEHLNFIIPATTSGCCRIIPSPDM 180  
DB 121 SCMGAPLHDDPFIIGIGKELIVNADSVTSFYPSAQOEHLNFIIPATTSGCCRIIPSPDM 180  
QY 181 SATHYCYTNHVLISGCRDHS HQYLALGVLTATGRIFFSTLRSISLDDTONRKSCSV 240  
DB 181 SATHYCYTNHVLISGCRDHS HQYLALGVLTATGRIFFSTLRSISLDDTONRKSCSV 240  
QY 241 SATPLGCDMLCSKYTEEBEDYNSAVPTMAHGRIGFDQYHEKLDVTTLPEDWYANP 300  
DB 241 SATPLGCDMLCSKYTEEBEDYNSAVPTMAHGRIGFDQYHEKLDVTTLPEDWYANP 300  
QY 301 GVGGSFIDGRVWFVSYYGGLKPNSSPDTVOEGKYIYKRYNDTCPEBODYQIRMAKSSYK 360  
DB 301 GVGGSFIDGRVWFVSYYGGLKPNSSPDTVOEGKYIYKRYNDTCPEBODYQIRMAKSSYK 360  
QY 361 PGRFGKRIQOAILSIKYSTSLGEBPVLTPPNTVTLMAEGRILTVGTSHPLYORGSY 420  
DB 361 PGRFGKRIQOAILSIKYSTSLGEBPVLTPPNTVTLMAEGRILTVGTSHPLYORGSY 420  
QY 421 FSPALLPYMTVSNKATLHSPYTFNAPTRPGSIPOCASARCPNSCTGYTDPYPLIFR 480  
DB 421 FSPALLPYMTVSNKATLHSPYTFNAPTRPGSIPOCASARCPNSCTGYTDPYPLIFR 480  
QY 481 NHTLRGVFGTMDSEQARLNPAASVPDSTRSRITRVSSTRAAYTSTCFKVVTKNTK 540  
DB 481 NHTLRGVFGTMDSEQARLNPAASVPDSTRSRITRVSSTRAAYTSTCFKVVTKNTK 540  
QY 541 YCLSTIAEISNTLFGERRIYPLVEILKNDGVREARSG 577  
DB 541 YCLSTIAEISNTLFGERRIYPLVEILKNDGVREARSG 577  
RESULT 11  
Q83844 PRELIMINARY; PRT; 577 AA.  
AC Q83844;  
DT 01-NOV-1996 (TREMBLrel. 01, Created)  
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)  
DE Hemagglutinin-neuraminidase.  
OS Newcastle disease virus.  
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;  
OC Paramyxoviridae; Paramyxovirinae; Rubulaviruses;  
OC NCBI\_TaxID=11176;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=vaccine 4;  
RX MEDLINE=96414821; PubMed=8817822;  
RA Seal B.S., King D.J., Bennett J.D.;  
RT "Characterization of Newcastle disease virus vaccines by biological properties and sequence analysis of the hemagglutinin-neuraminidase RT protein gene."  
RT Vaccine 14:761-766 (1996).  
RL EMBL; U37190; AAC55044.1; -  
DR InterPro; IPR000665; Hem-neuramidae.  
DR Pfam; PF00423; HN.1  
SQ SEQUENCE 577 AA; 63231 MW; ACC95422982CT878 CRC64;  
Query Match 96.3%; Score 2887; DB 12; Length 577;  
Best Local Similarity 95.7%; Pred. No. 2.5e-228;  
Matches 552; Conservative 12; Mismatches 13; Indels 0; Gaps 0;  
QY 1 MDRASQVLENDERBAKNTWRLIFRIAILLTVVTLATSVASLVYSGASTPSDLVGP 60  
DB 1 MDRASQVLENDERBAKNTWRLIFRIAILLTVVTLATSVASLVYSGASTPSDLVGP 60



Qy	61	RRISAAEERTALCSNOVDVRIKQVALLAESPLALNEMTTMNTISLSYQINGAANN	120
Dd	61	TRISAAEKRTISLSSNOVDVRYKQVLESPLALKETETPMNATISLSYQINGAANN	120
Qy	121	SGMGAPIHDPDPIGGIGKELIYDNASDVYSFYPSAFOEHLNFIAPATTSGSCRIPSPDM	180
Dd	121	SGMGAPIHDPDPIGGIGKELIYDDASDVYSFYPSAQOHLNFIAPATTSGSCRIRISFDM	180
Qy	181	SATHYCYTHNVILSGCRDHS HQYLALGVLTATAGRIFFSTLRISLDDTONRKSCSV	240
Dd	181	SATHYCYTHNVILSGCRDHS HQYISLGLRTSAGRVFESTLRISINLDDTONRKSCSV	240
Qy	241	SATPLGCMCLCSKATETEBEDYNSAVPTLMAGRGRLFDQYHEKDDVTLTFEDWYANP	300
Dd	241	SATPLGCMCLCSKVETEEDYNSAAPTMAGRGLRFDQYHEKDDVTLTFEDWYANP	300
Qy	301	GVGGGSFLDGRWFEVYGGLLKNSPBDTVQEGKYVLYKKRYNDPCPEBOYQIRMASSYK	360
Dd	301	GVGGGSFLDGRWFEVYGGLLKPNSPBDTVQEGKYVLYKKRYNDPCPEBOYQIRMASSYK	360
Qy	361	PGRFEGKRIQOAILISIKVSTSLGEPBVLTVPPNTVILMAEGRILVNGTSHFLYORGSSY	420
Dd	361	PGRFEGKRIQOAILISIKVSTSLGEPBVLTVPPNTVILMAEGRILVNGTSHFLYORGSSY	420
Qy	421	FSPALLYPMVYNSKNTATLHSPYTFNAFTRPGSIPCOASARCPNSCYTVATDPYPLIFXR	480
Dd	421	FSPALLYPMVYNSKNTATLHSPYTFNAFTRPGSIPCOASARCPNSCYTVATDPYPLIFXR	480
Qy	481	NHTLKGUVGTMLDSQOARLNPAASAVFDTSSRRIRTRVSSSTKYAAVYTSTCFKRVYTKNT	540
Dd	481	NHTLKGUVGTMLDSQOARLNPTSAVFDSTSSRRIRTRVSSSTKYAAVYTSTCFKRVYTKNT	540
Qy	541	YCLSLAEISNTLFGFRRIVPLLVETILKNDGVAEARG	577
Dd	541	YCLSLAEISNTLFGFRRIVPLLVETILKNDGVAEARG	577

RESULT 12			
063845			
ID	063845	PRELIMINARY;	PRT; 577 AA.
AC	063845;		
DT	01-NOV-1996 (TEMBLrel. 01, Created)		
DT	01-NOV-1996 (TEMBLrel. 01, Last sequence update)		
DT	01-JUN-2001 (TEMBLrel. 17, Last annotation update)		
DE	Hemagglutinin-neuraminidase.		
OS	Newcastle disease virus.		
OC	Viruses; ssRNA negative-strand viruses; Mononegavirales;		
OC	Paramyxoviridae; Paramyxovirinae; Rubulavirinae.		
OX	NCBI_TaxID=11176;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=Vaccine 5;		
RX	MEDLINE=96414821; PubMed=8817822;		
RA	Seal B.S., King D.J., Bennett J.D.;		
RT	"Characterization of Newcastle disease virus vaccines by biological		
RT	properties and sequence analysis of the hemagglutinin-neuraminidase		
RT	protein gene."		
RL	Vaccine 14:761-766(1996).		
DR	EMBL; U37191; AAC55045.1; -.		
DR	InterPro; IPR000665; Hem-neuramidae.		
DR	Pfam; PF00423; HN; 1.		
Q0	SEQUENCE 577 AA; 63409 MW; D8BF2C5EE1FDDCAD CRC64;		

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Query Match      96.3%; Score 2887; DB 12; Length 577;
Best Local Similarity 95.8%; Pred. No. 2.5e-22;
Matches 553; Conservative 10; Mismatches 14; Indels 0; Gaps 0;
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Dy

1 MDRAVSQVALLNDEKREAKTWRLIFRIAIILLITVTTLTTSVASLTYSMGASIPSDIQCIP 60  
||||| : ||||| :

Dd

1 MDRAVSQVALLNDEKREAKTWRLIFRIAILFLVTVTLLIASVLISLYSMGASTPSDLCVIP 60  
||||| : ||||| :

Oy

61 TRISAERKITSALGSNDVDRIYKVALLSPPLALLNTETTINMAITSLSYQINGAANN 120  
||||| : ||||| :

Db	6	TRISRAEKITSTLSGNDVDRIYKQVABEPLALNTETTINMAITSLSTQJNCAMANN	120
Oy	121	SGMGAPHDPEFIGIGIKBELIVDNASDVTSFYPSAPFOEHLNFI	180
Db	121	SGMGAPHDPEYIGIGIKBELIVDSDVTSFYPSAFOEHLNFI	180
Oy	181	SATXCYHANYILSGCRDSSHSHOVLALGVLTATNGRFPSFTLASISLDDJONRSCSV	240
Db	181	SATXCYHANYILSGCRDSSHSHOVLPLGLVLTATNGRFPSFTLASINDDJONRSCSV	240
Oy	241	SATPLGCDMLCSKOTETEEDYNSAVPTLMAHGRIGFDQYHEKDLVTTLFEDWVANY	300
Db	241	SATPLGCDMLCSKOTETEEDYNSAVPTRMWAGRIGFDQYHEKDLVTTLFEDWVANY	300
Oy	301	GVGGGSFIDGRVWVSYGVGLKPNSSPDVVOEKKVYIYKRYNDTCDEODYOIRMAKSSYK	360
Db	301	GVGGGSFIDSKVWVSYGVGLKPNSTSDVVOEKKVYIYKRYNDTCDEODYOIRMAKSSYK	360
Oy	361	PGRFGRKRIQOAILSIKVSITSLGEDPVLTVPNTVTLMGAEGRILTVGTSHEFLYORGSSY	420
Db	361	PRFRGGRRIQOAILSIKVSITSLGEEPPVLTVPNTVTLMGAEGRILTVGTSHEFLYORGSSY	420
Oy	421	FSPALLYPMYUSNKTATLHSPYTPAFPRPGSIPCOASARCNSCVTYGYPDPIEFR	480
Db	421	FSPALLYPMYUSNKTATLHSPYTPAFPRPGSIPCOASARCNSCVTYGYPDPIEFR	480
Oy	481	NHTLRGVGTMIDSEORALNPASAVFDSITSRSRITRVSSSSTKAAVYTTSCFVVTNXT	540
Db	481	NHTLRGVGTMIDSEORALNPASAVFDSITSRSRITRVSSSSTKAAVYTTSCFVVTNXT	540
Oy	541	YCLSTIAEISNLTFCGFRIVPLLVLTILKNDGVREASG	577
Db	541	HCLSTIAEISNLTFCGFRIVPLLVLTILKNDGVREASG	577

RESULT 13			
ID	Q9NCW3	PRELIMINARY;	PRT; 577 AA.
AC	Q9NCW3;		
DT	01-NOV-1999 (TREMBLrel. 12, Created)		
DT	01-NOV-1999 (TREMBLrel. 12, Last annotation update)		
DT	01-MAR-2002 (TREMBLrel. 20, Last annotation update)		
DE	Hemagglutinin-neuraminidase (EC 3.2.1.18).		
GN	HN		
OS	Newcastle disease virus.		
CC	Viruses; ssRNA negative-strand viruses; Mononegavirales;		
CC	Paramyxoviridae; Paramyxovirinae; Rubulavirinae.		
OX	NCBI_TaxID=11176;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RA	Sagresta A., Villar E.;		
RL	Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; AF098289; AAD28351.1; -		
DR	InterPro; IPR000665; Hem-neuramndase.		
DR	Pfam; PF00423; HN; 1.		
KW	Glycosidase; Hydrolase.		
SQ	SEQUENCE 577 AA; 63347 MW; 5673484C1B9ECCT CRC64;		

QY	1	MDRAVSQVLALENDREAKNTRLIFRIILLLTVTLTASVSLVYSGMAGSPSDLVGIP	60
QY	1	MDRAVSQVLALENDREAKNTRLIFRIILLLTVTLTASVSLVYSGMAGSPSDLVGIP	60
Db	1	MDRAVSQVLALENDREAKNTRLIFRIILLLTVTLTASVSLVYSGMAGSPSDLVGIP	60
QY	61	TRIRAEKITSAGSNQDVDRITYKQVALESPALLTETTIMAITSLSQINGAANN	120
Db	61	TRIRAEKITSAGSNQDVDRITYKQVALESPALLTETTIMAITSLSQINGAANN	120
QY	121	SGMGAPLHPDPFGIGIKELIVNADSDVTSFYPSAFQEHNLNIPAPTTGSGCCTRIIPSDM	180
Db	121	SGMGAPLHPDPFGIGIKELIVNADSDVTSFYPSAFQEHNLNIPAPTTGSGCCTRIIPSDM	180

Qy	181	SATHCYTHNYVILSGCRDHSNHOYALGVLTPTAAGRIFESTLRISLIDPDNRKSCSY	240
Qy	181	SATHCYTHNYVILSGCRDHSNHOYALGVLTPTAAGRIFESTLRISLIDPDNRKSCSY	240
Db	181	SATHCYTHNYVILSGCRDHSNHOYALGVLTPTAAGRIFESTLRISLIDPDNRKSCSY	240
Qy	241	SATPLGCDMLCSKVTETEEDEDYNSAVPTLMAHGRLOFDQYHEKDLDTVTTLFEDWANYP	300
Db	241	SATPLGCDMLCSKVTETEEDEDYNSAVPTLMAHGRLOFDQYHEKDLDTVTTLFEDWANYP	300
Qy	301	GVGGSSFLDGRWESVYGGILKPNSSBDTYQEGKTYVYKRYNDTCPEBDYQIRMASSSYK	360
Db	301	LVMGSSFLDSRWFSYVGGILKPNSSBDTYQEGKTYVYKRYNDTCPEBDYQIRMASSSYK	360
Qy	361	PGRFSGKRIQOAILISKVTSIGCEPVLTVPPNTVTLMAEGRILTVGSHFLYQGGSSY	420
Db	361	PGRFSGKRIQOAILISKVTSIGCEPVLTVPPNTVTLMAEGRILTVGSHFLYQGGSSY	420
Qy	421	FSPALLYEMTVSNKRTATLHSPYTFPNAFTRPGSIPCOASARCPNSCVYGYTDPYPLIFR	480
Db	421	FSPALLYEMTVSNKRTATLHSPYTFPNAFTRPGSIPCOASARCPNSCVYGYTDPYPLIFR	480
Qy	481	NHTLRGVGTMLDSQARLNPAASAVFDSRSRIRTVSSSSSTKAAVYTSICFKVCTNKY	540
Db	481	NHTLRGVGTMLDSQARLNPAASAVFDSRSRIRTVSSSSSTKAAVYTSICFKVCTNKY	540
Qy	541	YCLSTAEISNTLFGFGRVPLVLLVELIKNDGVNEARSG	577
Db	541	YCLSTAEISNTLFGFGRVPLVLLVELIKNDGVNEARSG	577

RESULT 14	ID	Q089712	PRELIMINARY;	PRT;	577 AA.
AC	Q089712;				
DT	01-NOV-1996	(TEMBLrel. 01, Created)			
DT	01-NOV-1996	(TEMBLrel. 01, last sequence update)			
DT	01-JUN-2001	(TEMBLrel. 17, last annotation update)			
DE	HEMAGGLUTININ-neuraminidase.				
OS	Newcastle disease virus.				
OC	viruses; ssRNA negative-strand viruses; Mononegavirales;				
OC	Paramyxoviridae; Paramyxovirinae; Rubulaviruses.				
OX	NCBI_Taxid=11176;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=VACCINE 6;				
RX	MEDLINE=96414821; Pubmed=8817822;				
RA	Seal B.S., King D.J., Bennett J.D.;				
RT	"Characterization of Newcastle disease virus vaccines by biological				
RT	properties and sequence analysis of the hemagglutinin-neuraminidase				
RT	protein gene.";				
RL	Vaccine 14:761-766(1996).				
DR	EMBL: U37192; AAC55046.1; -				
DR	EMBL: U37189; AAC55043.1; -				
DR	InterPro: IPR000665; Hem-neuraminde.				
DR	Pfam: PF00423; HN; 1.				
Q0	SEQUENCE 577 AA; 63401 MW; 1BBB6ED5DEDCD CEC64;				

Query Match	95.5%	Score 2863	DB 12	Length 577
Best Local Similarity	95.3%	Pred. No. 2.4e-226		
Matches 550, Conservative	12	Mismatches 15	Indels 0	Gaps 0

Qy	1	MDRAVSQVALENDDEEAKNTWRLFRIRALLTLVTVAIVASVLSVMSASPSDVLVGP	60
Db	1	MDRAVSQVALENDDEEAKNTWRLFRIRALLTLVTVAIVASVLSVMSASPSDVLVGP	60
Qy	61	TRISAEEKITSALECSNODVNDRIKQVVALESPALINNETTIMANITSLVQINAAAN	120
Db	61	TRISAEEKITSLTSSNODVNDRIKQVVALESPALINNETTIMANITSLVQINAAAN	120
Qy	121	SGMGAPIHDPDPIGGIGKELIVDNASDVTSFPYPSAFQEHINFI PAVTTSGGCRIRPSFDM	180
Db	121	SGMGAPIHDPDPIGGIGKELIVDNASDVTSFPYPSAFQEHINFI PAVTTSGGCRIRPSFDM	180

QY	181	SATHCYHNYILSCCRDHHSHOYLAQVATTNGRIFSTLSISLDDPNRSCSV	240
Db	181	SATHDCYHNYILSCCRDHHSHOYLAQVARTSATGRVFBTILSINDDPNRSCSV	240
QY	241	SATPLGCDMLCSKVETEEDBYNDAVPTLMAHGRIGFDQYHEKDLVTTLFEDWVANY	300
Db	241	SATPLGCDMLCSKVETEEDBYNDAVPTRMVHGRIGFDQYHEKDLVTTLFGDWVANY	300
QY	301	GVGGSSFLDGRVWFSVYGGIKPNASBDTYOBEKVYIYKRYNNTCCDEDOYQIRMASSYK	360
Db	301	GVGGSSFLDSRWFWFSVYGGIKPNTSDTYOBEKVYIYKRYNNTCCDEDOYQIRMASSYK	360
QY	361	PGRFSGKRIQOAILISIKVTSLGEDEPVLTPPNTATLMAGBERILTVGSHFLYQRGSSY	420
Db	361	PGRFSGKRIQOAILISIKVTSLGEDEPVLTPPNTATLMAGBERILTVGSHFLYQRGSSY	420
QY	421	FSPALLYEMTVSNKATATLHSPYTFNAFTRPGSIPCOASARCENSCVGYTDPYPLIFR	480
Db	421	FSPALLYEMTVSNKATATLHSPYTFNAFTRPGSIPCOASARCENSCVGYTDPYPLIFR	480
QY	481	NHTLRGVFTMLDSQARLNPASAVFDSTSRIRTRVSSSTKAAVYTTSTCRVVKTNKT	540
Db	481	NHTLRGVFTMLDSQARLNPASAVFDSTSCSIRIRVSPSTSKAAVYTTSTCRVVKTNKT	540
QY	541	YCLSLAIESTNLTFFGEFRIVPLLVETLKNDDGYREARSG	577
Db	541	YCLSLAIESTNLTFFGEFRIVPLLVETLKNDDGYREARSG	577

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RESULT 15
083843
ID 083843 PRELIMINARY; PRT; 577 AA.
AC 083843;
DT 01-NOV-1996 (TEMBLrel. 01, Created)
DT 01-NOV-1996 (TEMBLrel. 01, last sequence update)
DI 01-JUN-2001 (TEMBLrel. 17, last annotation update)
DE Hemagglutinin-neuraminidase.
OS Newcastle disease virus.
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Paramyxoviridae; Paramyxovirinae; Rubulavirus.
CX NCBI_TaxID=11176;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=vaccine 2;
RX MEDLINE=96414821; Pubmed=8817822;
RA Seal B.S., King D.J., Bennett J.D.;
RT "Characterization of Newcastle disease virus vaccines by biological
RT properties and sequence analysis of the hemagglutinin-neuraminidase
RT protein gene.";
RL Vaccine 14:761-766(1996).
DR EMBL: U37188; AAC55042.1; -.
DR InterPro: IPR000665; Hem-neuramidae.
DR Pfam: PF00423; HN; 1.
SQ SEQUENCE 577 AA; 63174 MW; E3241EDB48B4CB33 CRC64;

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Query Match	95.4%	Score 2860	DB 12	Length 577
Best Local Similarity	95.1%	Pred. NO. 4.2e-226		
Matches 549	10	Mismatches 18	Indels 0	Gaps 0

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Db	1	MDRAVSQVALENDEEAEANTWRLIFRIAILFLVTTLAISVASLISYMGASPSDVLGIP	60
QY	61	TRISAEKITSALGSNOVDVRIYKQVALESPLALNTETTIMAITSLSYQINGAANN	120
Db	61	TRISAEKITSYLGSNQVDVRLKYQVALESPLALLTETTIMAITSLSYQINGAANN	120
QY	121	SGMGAPHIDDPFIGIGIKELIYDNASDVTSFSPSAFOEHLNFIIPATGSGGCRJIPSFM	180
Db	121	SGMGAPHIDDPYIGIGIKELIYDDASDVTSFSPSASQOOLNFIIPATGSGGCRJIPSPFM	180
QY	181	SATHCYTHANITLSCGRDHSNHOVLALGVLRRTATGRIFPFTLSISLSDDTQNRKSGSV	240

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Db 181 SATQCYTHNVILSCCRDHSYQYISIGVLTSAIGRVFSTLRSINLDDTQNRKSCSV 240
Qy 241 SATPLGCDMLCSKYETEEDYNSAVPTLMAHGRIGFDQYHEKDLDTTLFEDWVANYP 300
Db 241 SATPLGCDMLCSKYETEEDYNSAVPTLMAHGRIGFDQYHEKDLDTTLFEDWVANYP 300
Qy 301 GVGGSFIDGRVWFSVYGGKPNSPDYOEGKYIYKRYNDTCPEODYOIRMAKSSYK 360
Db 301 GVGGSFIDSRVWFSYGGKPNSPDYOEGKYIYKRYNDTCPEODYOIRMAKSSYK 360
Qy 361 PGRFGKRIOQAILISIKVSTSLGEDPVLTPPNTVTLMGAEGRILTVGSHFLYORGSSY 420
Db 361 PGRFGKRIOQAILISIKVSTSLGEDPVLTPPNTVTLMGAEGRILTVGSHFLYORGSSY 420
Qy 421 FSPALLYPMYVSNKATATLHSPYTFNAFTRPCSIPCOASARCPNSCVTGVTDPYPLIFR 480
Db 421 FSPALLYPMYVSNKATATLHSPYTFNAFTRPCSIPCOASARCPNSCVTGVTDPYPLIFR 480
Qy 481 NHTLRGVFGTMDSEQARLNPASAVFDSSTSRRTTRVSSSTKAAYTTSTCFKVVKTNT 540
Db 481 NHTLRGVFGTMDGVQARLNPASAVFDSSTSRRTTRVSSSTKAAYTTSTCFKVVKTNT 540
Qy 541 YCLSTABISNTLFGFRIVPLLVEILKNDGVREARSG 577
Db 541 YCLSTABISNTLFGFRIVPLLVEILKNDGVREARSG 577
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Job time : 67 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 2, 2004, 16:16:51 ; Search time 18 Seconds  
(without alignments)  
1356.298 Million cell updates/sec

Title: US-09-915-515A-1

Perfect score: 2998  
Sequence: 1 MDRVSOVALENDREKAKNT.....IVPLVETLKNVDGVEARSG 577

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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2: /cgn2\_6/ptodata/2/1aa/5B.COMB.pep: \*  
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4: /cgn2\_6/ptodata/2/1aa/6B.COMB.pep: \*  
5: /cgn2\_6/ptodata/2/1aa/PTUS.COMB.pep: \*  
6: /cgn2\_6/ptodata/2/1aa/backfile1.pep: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2970	99.1	577	6 5310678-3	Patent No. 5310678
2	2920	97.4	577	1 US-07-820-154A-30	Sequence 30, Appl
3	2920	97.4	577	2 US-08-663-566A-11	Sequence 11, Appl
4	2920	97.4	577	2 US-08-097-554A-30	Sequence 30, Appl
5	2920	97.4	577	2 US-08-023-610-11	Sequence 11, Appl
6	2920	97.4	577	2 US-08-288-065A-11	Sequence 11, Appl
7	2920	97.4	577	2 US-08-362-240A-11	Sequence 11, Appl
8	2920	97.4	577	3 US-08-480-640A-30	Sequence 30, Appl
9	2920	97.4	577	3 US-08-295-802-30	Sequence 30, Appl
10	2920	97.4	577	3 US-08-804-372A-9	Sequence 9, Appl
11	2920	97.4	577	3 US-08-488-237A-30	Sequence 30, Appl
12	2920	97.4	577	4 US-08-375-992A-30	Sequence 30, Appl
13	2920	97.4	577	4 US-08-472-679H-30	Sequence 30, Appl
14	2920	97.4	577	5 PCT-US93-100324-30	Sequence 30, Appl
15	2920	97.4	577	5 PCT-US95-10245-11	Sequence 11, Appl
16	2915	97.2	581	2 US-08-484-575A-13	Sequence 13, Appl
17	2915	97.2	581	3 US-08-477-459-13	Sequence 13, Appl
18	2915	97.2	581	3 US-08-479-869-13	Sequence 13, Appl
19	2915	97.2	581	3 US-08-486-414-13	Sequence 13, Appl
20	2915	97.2	581	5 PCT-US94-01836A-13	Sequence 13, Appl
21	2915	97.2	581	5 PCT-US94-02252A-13	Sequence 13, Appl
22	2750	91.7	571	1 US-08-368-803-17	Sequence 17, Appl
23	2716.5	90.6	569	4 US-09-362-831-9	Sequence 9, Appl
24	765	25.5	565	2 US-08-700-548-2	Sequence 2, Appl
25	449	15.0	572	1 US-08-191-866D-81	Sequence 81, Appl
26	449	15.0	572	2 US-08-185-949B-81	Sequence 81, Appl
27	444.5	14.8	572	3 US-08-987-439-3	Sequence 3, Appl

28	442.5	14.8	572	2 US-08-467-963C-4	Sequence 4, Appl
29	442.5	14.8	572	2 US-08-838-189D-4	Sequence 4, Appl
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34	442.5	14.8	572	3 US-08-001-554A-4	Sequence 4, Appl
35	119	4.0	1198	4 US-09-199-637A-405	Sequence 405, Appl
36	112	3.7	28	3 US-08-486-414-35	Sequence 35, Appl
37	102.5	3.4	1170	4 US-09-749-588-2	Sequence 2, Appl
38	101.5	3.4	1146	4 US-09-198-452A-580	Sequence 580, Appl
39	100.5	3.4	1752	4 US-09-865-621A-2	Sequence 2, Appl
40	99.5	3.3	650	3 US-08-362-525-2	Sequence 2, Appl
41	99	3.3	766	4 US-09-328-352-8230	Sequence 8230, Appl
42	97.5	3.3	804	4 US-09-328-352-5545	Sequence 5545, Appl
43	96	3.2	3892	4 US-09-328-352-5503	Sequence 5503, Appl
44	95.5	3.2	1584	3 US-09-251-645-6	Sequence 6, Appl
45	94	3.1	377	1 US-07-772-087-2	Sequence 2, Appl

ALIGNMENTS

RESULT 1									
5310678-3									
: Patent No. 5310678									
: Applicant: Bingham, Richard W.; Chambers, Philip; Emerson, Peter									
: T. Millar, Neil S.									
: TITLE OF INVENTION: NEWCASTLE DISEASE VIRUS GENE CLONES									
: NUMBER OF SEQUENCES: 3									
: CURRENT APPLICATION DATA: US/07/438,945									
: FILING DATE: 17-NOV-1989									
: PRIOR APPLICATION DATA:									
: APPLICATION NUMBER: 885,765									
: FILING DATE: 15-JUL-1986									
: SEQ ID NO:3:									
: LENGTH: 577									
5310678-3									
Query Match 99.1%; Score 2970; DB 6; Length 577;									
Best Local Similarity 99.1%; Pred. No. 3.2e-300;									
Matches 572; Conservative 2; Mismatches 3; Indels 0; Gaps 0;									
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QY	61	TRISRAEKTISALGSNOVDVDRILYKOVALLSPALINTETTINMAITSLSYQINGAANN	120						
DB	61	TRISRAEKTISALGSNOVDVDRILYKOVALLSPALINTETTINMAITSLSYQINGAANN	120						
QY	121	SGWGAIPHDPFIFGIGIKELIVDNASDVTSFYPFAFOEHLNFIAPPTGSGCTRI	180						
DB	121	SGWGAIPHDPFIFGIGIKELIVDNASDVTSFYPFAFOEHLNFIAPPTGSGCTRI	180						
QY	181	SATHYCTHNVITLGGCRDHSNHOYALGVLTATATGRIFPSTIRSLDPTORRKS	240						
DB	181	SATHYCTHNVITLGGCRDHSNHOYALGVLTATATGRIFPSTIRSLDPTORRKS	240						
QY	241	SATPLGCDMLCKSTETREEDYNSAVPTLMAHGLGFGGOVHEKDLVTTLFEEDVANY	300						
DB	241	SATPLGCDMLCKSTETREEDYNSAVPTLMAHGLGFGGOVHEKDLVTTLFEEDVANY	300						
QY	301	GVGGGSFIDGRWMSVYGLKPNPSPTDVGKVIYIKRYNDPCPDQDYOIRAKSKSY	360						
DB	301	GVGGGSFIDGRWMSVYGLKPNPSPTDVGKVIYIKRYNDPCPDQDYOIRAKSKSY	360						
QY	361	PGRRGKRIQOALISIVKSTLSGDPVLTPVPNTVLMAGARILTYGTSPFLYQSGSY	420						
DB	361	PGRRGKRIQOALISIVKSTLSGDPVLTPVPNTVLMAGARILTYGTSPFLYQSGSY	420						
QY	421	FSPALVPMVTSNKTATLHSPYTFNAFTRPGSICQASARCPCNCSVGVYDPPFLFYR	480						

Db 421 FSPALLPYMTVSNKXTALHSPYTFNAFTPRGSI PCQASARCPNSCVTVTDEPILFYR 480  
QY 481 NHTLRGVFGTMDSEQARLNPAASVPDSTSRSTRTRVSSSTKAAYTSTCFVVKTKNT 540  
Db 481 NHTLRGVFGTMDSEQARLNPAASVPDSTSRSTRTRVSSSTKAAYTSTCFVVKTKNT 540  
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RESULT 2  
US-07-820-154A-30

/ Sequence 30, Application US/07820154A  
/ Patent No. 5382425  
/ GENERAL INFORMATION:  
/ APPLICANT: Cochran Ph. D., Mark D  
/ APPLICANT: Junker M.S., David B  
/ TITLE OF INVENTION: Recombinant Swinepox Virus  
/ NUMBER OF SEQUENCES: 40  
/ CORRESPONDENCE ADDRESS:  
/ ADDRESSEE: John P. White  
/ STREET: 30 Rockefeller Plaza  
/ CITY: New York  
/ STATE: New York  
/ COUNTRY: USA  
/ ZIP: 10112  
/ COMPUTER READABLE FORM:  
/ MEDIUM TYPE: Floppy disk  
/ COMPUTER: IBM PC compatible  
/ OPERATING SYSTEM: PC-DOS/MS-DOS  
/ SOFTWARE: Patent in Release #1.0, Version #1.25  
/ CURRENT APPLICATION DATA:  
/ APPLICATION NUMBER: US/07/820.154A  
/ FILING DATE: 19920113  
/ CLASSIFICATION: 424  
/ ATTORNEY/AGENT INFORMATION:  
/ NAME: White, John P  
/ TELEPHONE: (212)977-9550  
/ TELEFAX: (212)664-0525  
/ TELEX: 422523  
/ INFORMATION FOR SEQ ID NO: 30:  
/ SEQUENCE CHARACTERISTICS:  
/ LENGTH: 577 amino acids  
/ TYPE: AMINO ACID  
/ TOPOLOGY: linear  
/ MOLECULE TYPE: protein  
/ US-07-820-154A-30

Query Match 97.4%; Score 2920; DB 1; Length 577;  
Best Local Similarity 96.9%; Pred. No. 5.1e-295;  
Matches 559; Conservative 8; Mismatches 10; Indels 0; Gaps 0;

QY 1 MDRASQVALENDEREAKNTWRLIFRIAILLVVTATVSLVSMGASTSDLVGIP 60  
Db 1 MDRASQVALENDEREAKNTWRLIFRIAILLVVTATVSLVSMGASTSDLVGIP 60  
QY 61 TRISRAEEKITSALGSNOVDVDRIRYQVALESPLALNTETIMNAITSLSYQINGAANN 120  
Db 61 TRISRAEEKITSALGSNOVDVDRIRYQVALESPLALNTETIMNAITSLSYQINGAANN 120  
QY 121 SGMGAPRHHDDPFGIGIKELIVNADSVTSFYPSAFQEHNFIPAPPTGSGCRRIPSDM 180  
Db 121 SGMGAPRHHDDPFGIGIKELIVNADSVTSFYPSAFQEHNFIPAPPTGSGCRRIPSDM 180  
QY 181 SATHYCTYHNVVILSGCRDHSRHOYLALGVLRATATGRIFPSTLSISLDTQNRKSCSV 240  
Db 181 SATHYCTYHNVVILSGCRDHSRHOYLALGVLRATATGRIFPSTLSISLDTQNRKSCSV 240  
QY 241 SATPLGCDMLCSKATETEEDYNSAVPTLMAHGRIGFDQYHEKOLDVTTLFEDWVANYP 300  
Db 241 SATPLGCDMLCSKATETEEDYNSAVPTLMAHGRIGFDQYHEKOLDVTTLFEDWVANYP 300

Db 241 SATPLGCDMLCSKATETEEDYNSAVPTLMAHGRIGFDQYHEKOLDVTTLFEDWVANYP 300  
QY 301 GVGGSGFIDGRVWFVSYYGGLKPNSPEDTVQEGKVYIKKYNPTCPDEOPYOIRMAKSSYK 360  
Db 301 GVGGSGFIDGRVWFVSYYGGLKPNSPEDTVQEGKVYIKKYNPTCPDEOPYOIRMAKSSYK 360  
QY 361 PGRFGGKRIQOAILISIKVSTSLGEBDVLTPPVYTLTMAGRILTVGTSHPLYQSGSY 420  
Db 361 PGRFGGKRIQOAILISIKVSTSLGEBDVLTPPVYTLTMAGRILTVGTSHPLYQSGSY 420  
QY 421 FSPALLPYMTVSNKXTALHSPYTFNAFTPRGSI PCQASARCPNSCVTVTDEPILFYR 480  
Db 421 FSPALLPYMTVSNKXTALHSPYTFNAFTPRGSI PCQASARCPNSCVTVTDEPILFYR 480  
QY 481 NHTLRGVFGTMDSEQARLNPAASVPDSTSRSTRTRVSSSTKAAYTSTCFVVKTKNT 540  
Db 481 NHTLRGVFGTMDSEQARLNPAASVPDSTSRSTRTRVSSSTKAAYTSTCFVVKTKNT 540  
QY 541 YCLSIASISNTLFGFRIVPLVLEILKNDGVREARSG 577  
Db 541 YCLSIASISNTLFGFRIVPLVLEILKNDGVREARSG 577

RESULT 3  
US-08-663-566A-11

/ Sequence 11, Application US/08663566A  
/ Patent No. 5853733  
/ GENERAL INFORMATION:  
/ APPLICANT: Cochran, Mark D  
/ APPLICANT: Macdonald, Richard D  
/ TITLE OF INVENTION: Recombinant Herpesvirus of Turkeys  
/ NUMBER OF SEQUENCES: 56  
/ CORRESPONDENCE ADDRESS:  
/ ADDRESSEE: John P. White  
/ STREET: 1185 Avenue of the Americas  
/ CITY: New York  
/ STATE: New York  
/ COUNTRY: USA  
/ ZIP: 10036  
/ COMPUTER READABLE FORM:  
/ MEDIUM TYPE: Floppy disk  
/ COMPUTER: IBM PC compatible  
/ OPERATING SYSTEM: PC-DOS/MS-DOS  
/ SOFTWARE: Patent in Release #1.0, Version #1.25  
/ CURRENT APPLICATION DATA:  
/ APPLICATION NUMBER: US/08/663.566A  
/ FILING DATE: June 13, 1996  
/ CLASSIFICATION: 435  
/ ATTORNEY/AGENT INFORMATION:  
/ NAME: White, John P  
/ TELEPHONE: (212)278-0400  
/ TELEFAX: (212)391-0526  
/ TELEX: 422523  
/ INFORMATION FOR SEQ ID NO: 11:  
/ SEQUENCE CHARACTERISTICS:  
/ LENGTH: 577 amino acids  
/ TYPE: amino acid  
/ TOPOLOGY: linear  
/ MOLECULE TYPE: protein  
/ US-08-663-566A-11

Query Match 97.4%; Score 2920; DB 2; Length 577;  
Best Local Similarity 96.9%; Pred. No. 5.1e-295;  
Matches 559; Conservative 8; Mismatches 10; Indels 0; Gaps 0;

QY 1 MDRASQVALENDEREAKNTWRLIFRIAILLVVTATVSLVSMGASTSDLVGIP 60  
Db 1 MDRASQVALENDEREAKNTWRLIFRIAILLVVTATVSLVSMGASTSDLVGIP 60  
QY 61 TRISRAEEKITSALGSNOVDVDRIRYQVALESPLALNTETIMNAITSLSYQINGAANN 120  
Db 61 TRISRAEEKITSALGSNOVDVDRIRYQVALESPLALNTETIMNAITSLSYQINGAANN 120

Db 61 TRISRAEKTSTLGSNODVDRIRYKQVLESPLALNTETTINMATTSLSYOINGANN 120  
Qy 121 SGWGAPIHDPPIGIGIKELIVDNASVTSFYPSAFQEHNFIPAPTTGSGCTRIPSFDM 180  
Db 121 SGWGAPIHDPPIGIGIKELIVDNASVTSFYPSAFQEHNFIPAPTTGSGCTRIPSFDM 180  
Qy 181 SATHYCYTHNVILSGCRDHS HQYALGVLRRTATGRIFPSTLRSISLDDTONRKSCSV 240  
Db 181 SATHYCYTHNVILSGCRDHS HQYALGVLRRTATGRIFPSTLRSISLDDTONRKSCSV 240  
Qy 241 SATPLGCDMLCSKATEEEDDYNASVPTLMAHGRGLGPDQYHEKDLVTTLPEDWVANYP 300  
Db 241 SATPLGCDMLCSKATEEEDDYNASVPTLMAHGRGLGPDQYHEKDLVTTLPEDWVANYP 300  
Qy 301 GVGGGSFIDGRWVPSVYVGLKPNPSPTVOEGKVIYKRYNDTCPEBDYOIRMAKSSYK 360  
Db 301 GVGGGSFIDGRWVPSVYVGLKPNPSPTVOEGKVIYKRYNDTCPEBDYOIRMAKSSYK 360  
Qy 361 PGRFGKRIQOAILSIKYSTSLGEDPVLTPPNTVTLMAGGRLLTVGTSHFLYQRGSSY 420  
Db 361 PGRFGKRIQOAILSIKYSTSLGEDPVLTPPNTVTLMAGGRLLTVGTSHFLYQRGSSY 420  
Qy 421 FSPALLPMTVSNKTATLHSPYTFNAFTRPQSIPOQASARCPNSCVTVTDPPYLI FYR 480  
Db 421 FSPALLPMTVSNKTATLHSPYTFNAFTRPQSIPOQASARCPNSCVTVTDPPYLI FYR 480  
Qy 481 NHTLRGVFGTMDSEORLNPASAVFDSRSRTTRVSSSTKAAYTSTCFKVKTKNT 540  
Db 481 NHTLRGVFGTMDSEORLNPASAVFDSRSRTTRVSSSTKAAYTSTCFKVKTKNT 540  
Qy 541 YCLSIABISNTLFGFPRIVPLVLEILKNDGVREARSG 577  
Db 541 YCLSIABISNTLFGFPRIVPLVLEILKNDGVREARSG 577

RESULT 4  
US-08-097-554A-30  
Sequence 30, Application US/08097554A  
Patent No. 5869312  
GENERAL INFORMATION:  
APPLICANT: Cochran Ph.D., Mark D  
APPLICANT: Junker M.S., David E  
TITLE OF INVENTION: Recombinant Swinepox Virus  
NUMBER OF SEQUENCES: 112  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: John P. White  
STREET: 30 Rockefeller Plaza  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10112  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/097,554A  
FILING DATE: July 22, 1993  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: White, John P  
TELEPHONE: (212)977-9550  
TELEFAX: (212)664-0525  
TELETYPE: 422523  
INFORMATION FOR SEQ ID NO: 30:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 577 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein

US-08-097-554A-30  
Query Match 97.4%; Score 2920; DB 2; Length 577;  
Best Local Similarity 96.9%; Pred. No. 5,1e-295;  
Matches 559; Conservative 8; Mismatches 10; Indels 0; Gaps 0;

Qy 1 MDRAVSQVALLENDERAKNTWRLIFRIAILLVTLATSVASLVYMGASTPSDLVGIP 60  
Db 1 MDRAVSQVALLENDERAKNTWRLIFRIAILLVTLATSVASLVYMGASTPSDLVGIP 60  
Qy 61 TRISRAEKTSTLGSNODVDRIRYKQVLESPLALNTETTINMATTSLSYOINGANN 120  
Db 61 TRISRAEKTSTLGSNODVDRIRYKQVLESPLALNTETTINMATTSLSYOINGANN 120  
Qy 121 SGWGAPIHDPPIGIGIKELIVDNASVTSFYPSAFQEHNFIPAPTTGSGCTRIPSFDM 180  
Db 121 SGWGAPIHDPPIGIGIKELIVDNASVTSFYPSAFQEHNFIPAPTTGSGCTRIPSFDM 180  
Qy 181 SATHYCYTHNVILSGCRDHS HQYALGVLRRTATGRIFPSTLRSISLDDTONRKSCSV 240  
Db 181 SATHYCYTHNVILSGCRDHS HQYALGVLRRTATGRIFPSTLRSISLDDTONRKSCSV 240  
Qy 241 SATPLGCDMLCSKATEEEDDYNASVPTLMAHGRGLGPDQYHEKDLVTTLPEDWVANYP 300  
Db 241 SATPLGCDMLCSKATEEEDDYNASVPTLMAHGRGLGPDQYHEKDLVTTLPEDWVANYP 300  
Qy 301 GVGGGSFIDGRWVPSVYVGLKPNPSPTVOEGKVIYKRYNDTCPEBDYOIRMAKSSYK 360  
Db 301 GVGGGSFIDGRWVPSVYVGLKPNPSPTVOEGKVIYKRYNDTCPEBDYOIRMAKSSYK 360  
Qy 361 PGRFGKRIQOAILSIKYSTSLGEDPVLTPPNTVTLMAGGRLLTVGTSHFLYQRGSSY 420  
Db 361 PGRFGKRIQOAILSIKYSTSLGEDPVLTPPNTVTLMAGGRLLTVGTSHFLYQRGSSY 420  
Qy 421 FSPALLPMTVSNKTATLHSPYTFNAFTRPQSIPOQASARCPNSCVTVTDPPYLI FYR 480  
Db 421 FSPALLPMTVSNKTATLHSPYTFNAFTRPQSIPOQASARCPNSCVTVTDPPYLI FYR 480  
Qy 481 NHTLRGVFGTMDSEORLNPASAVFDSRSRTTRVSSSTKAAYTSTCFKVKTKNT 540  
Db 481 NHTLRGVFGTMDSEORLNPASAVFDSRSRTTRVSSSTKAAYTSTCFKVKTKNT 540  
Qy 541 YCLSIABISNTLFGFPRIVPLVLEILKNDGVREARSG 577  
Db 541 YCLSIABISNTLFGFPRIVPLVLEILKNDGVREARSG 577

RESULT 5  
US-08-023-610-11  
Sequence 11, Application US/08023610  
Patent No. 5926648  
GENERAL INFORMATION:  
APPLICANT: Cochran Ph.D., Mark D  
APPLICANT: Macdonald Ph.D., Richard D  
TITLE OF INVENTION: Recombinant Herpesvirus of Turkey  
NUMBER OF SEQUENCES: 47  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: John P. White  
STREET: 30 Rockefeller Plaza  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10112  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/023,610  
FILING DATE: February 26, 1993  
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:  
NAME: White Esq, John P  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212)977-9550  
TELEFAX: (212)664-0525  
TELEX: 422523  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 577 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-023-610-11

Query Match 97.4%; Score 2920; DB 2; Length 577;  
Best Local Similarity 96.9%; Pred. No. 5.1e-295;  
Matches 559; Conservative 8; Mismatches 10; Indels 0; Gaps 0;

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QY 1 MDRAVQVALENDERAKNTWRLIFRIAILLTVVTLATSVASLYSMGASTPSDLVGIP 60
DB 1 MDRAVQVALENDERAKNTWRLIFRIAILLTVVTLATSVASLYSMGASTPSDLVGIP 60
QY 61 TRISRAEEKITSLAGSNQDVDRIRYKQVVALESPALINTEITTMATISLSTQINGAANN 120
DB 61 TRISRAEEKITSLAGSNQDVDRIRYKQVVALESPALINTEITTMATISLSTQINGAANN 120
QY 121 SGMGAPRHDPDFIGIGKELIVDNASDVTSFYPSAFOEHLNFIAPPTTSGCTRIIPSDM 180
DB 121 SGMGAPRHDPDFIGIGKELIVDNASDVTSFYPSAFOEHLNFIAPPTTSGCTRIIPSDM 180
QY 181 SATHYCYTHNVILSGCRDHS HQYLALGVLRRTATGRIFSTLRSISLDDTONRKSCSV 240
DB 181 SATHYCYTHNVILSGCRDHS HQYLALGVLRRTATGRIFSTLRSISLDDTONRKSCSV 240
QY 241 SATPLGCDMLCSKATTEBEDYNSAVPTMAHGRGFDQYHEKLDVTLTFEDWVANYP 300
DB 241 SATPLGCDMLCSKATTEBEDYNSAVPTMAHGRGFDQYHEKLDVTLTFEDWVANYP 300
QY 301 GVGGSFIDGRWVFSYVGLKPNPSDVOEGKVIYKRYNDTCPEODYQIRMAKSSYK 360
DB 301 GVGGSFIDGRWVFSYVGLKPNPSDVOEGKVIYKRYNDTCPEODYQIRMAKSSYK 360
QY 361 PGRFGKRIQOAILSIKVTSLGEDPVLTPPNTVTLMAEGRIILVTGSHFLYQSGSSY 420
DB 361 PGRFGKRIQOAILSIKVTSLGEDPVLTPPNTVTLMAEGRIILVTGSHFLYQSGSSY 420
QY 421 FSPALLYPMVTSNKTATLHSPYTFNAFTPGSIPCOASARCPNSCVTYTDPYPLIFR 480
DB 421 FSPALLYPMVTSNKTATLHSPYTFNAFTPGSIPCOASARCPNSCVTYTDPYPLIFR 480
QY 481 NHTLRGVFGTMDSEARLNPAASAVPSTSRSTRTRVSSSTKAAVTTSTCFKVVTKNTK 540
DB 481 NHTLRGVFGTMDSEARLNPAASAVPSTSRSTRTRVSSSTKAAVTTSTCFKVVTKNTK 540
QY 541 YCLSLAIEISNTLFGFRIIVPLVLEILKNDGVREARSG 577
DB 541 YCLSLAIEISNTLFGFRIIVPLVLEILKNDGVREARSG 577
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RESULT 6  
US-08-288-065A-11  
Sequence 11. Application US/08288065A  
Patent No. 5961982  
GENERAL INFORMATION:  
APPLICANT: Cochran, Mark D  
APPLICANT: Macdonald, Richard D  
TITLE OF INVENTION: Recombinant Herpesvirus of Turkey's S-  
TITLE OF INVENTION: HVT-050 and Uses Thereof  
NUMBER OF SEQUENCES: 56  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: John P. White  
STREET: 1185 Avenue of the Americas  
CITY: New York

STATE: New York  
COUNTRY: USA  
ZIP: 10036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/288,065A  
FILING DATE: Aug-09-94  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: White, John P  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212)278-0400  
TELEFAX: (212)391-0526  
TELEX: 422523  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 577 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-288-065A-11

Query Match 97.4%; Score 2920; DB 2; Length 577;  
Best Local Similarity 96.9%; Pred. No. 5.1e-295;  
Matches 559; Conservative 8; Mismatches 10; Indels 0; Gaps 0;

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QY 1 MDRAVQVALENDERAKNTWRLIFRIAILLTVVTLATSVASLYSMGASTPSDLVGIP 60
DB 1 MDRAVQVALENDERAKNTWRLIFRIAILLTVVTLATSVASLYSMGASTPSDLVGIP 60
QY 61 TRISRAEEKITSLAGSNQDVDRIRYKQVVALESPALINTEITTMATISLSTQINGAANN 120
DB 61 TRISRAEEKITSLAGSNQDVDRIRYKQVVALESPALINTEITTMATISLSTQINGAANN 120
QY 121 SGMGAPRHDPDFIGIGKELIVDNASDVTSFYPSAFOEHLNFIAPPTTSGCTRIIPSDM 180
DB 121 SGMGAPRHDPDFIGIGKELIVDNASDVTSFYPSAFOEHLNFIAPPTTSGCTRIIPSDM 180
QY 181 SATHYCYTHNVILSGCRDHS HQYLALGVLRRTATGRIFSTLRSISLDDTONRKSCSV 240
DB 181 SATHYCYTHNVILSGCRDHS HQYLALGVLRRTATGRIFSTLRSISLDDTONRKSCSV 240
QY 241 SATPLGCDMLCSKATTEBEDYNSAVPTMAHGRGFDQYHEKLDVTLTFEDWVANYP 300
DB 241 SATPLGCDMLCSKATTEBEDYNSAVPTMAHGRGFDQYHEKLDVTLTFEDWVANYP 300
QY 301 GVGGSFIDGRWVFSYVGLKPNPSDVOEGKVIYKRYNDTCPEODYQIRMAKSSYK 360
DB 301 GVGGSFIDGRWVFSYVGLKPNPSDVOEGKVIYKRYNDTCPEODYQIRMAKSSYK 360
QY 361 PGRFGKRIQOAILSIKVTSLGEDPVLTPPNTVTLMAEGRIILVTGSHFLYQSGSSY 420
DB 361 PGRFGKRIQOAILSIKVTSLGEDPVLTPPNTVTLMAEGRIILVTGSHFLYQSGSSY 420
QY 421 FSPALLYPMVTSNKTATLHSPYTFNAFTPGSIPCOASARCPNSCVTYTDPYPLIFR 480
DB 421 FSPALLYPMVTSNKTATLHSPYTFNAFTPGSIPCOASARCPNSCVTYTDPYPLIFR 480
QY 481 NHTLRGVFGTMDSEARLNPAASAVPSTSRSTRTRVSSSTKAAVTTSTCFKVVTKNTK 540
DB 481 NHTLRGVFGTMDSEARLNPAASAVPSTSRSTRTRVSSSTKAAVTTSTCFKVVTKNTK 540
QY 541 YCLSLAIEISNTLFGFRIIVPLVLEILKNDGVREARSG 577
DB 541 YCLSLAIEISNTLFGFRIIVPLVLEILKNDGVREARSG 577
```

RESULT 7  
US-08-362-240A-11



Sequence 11, Application US/08362240A  
Patent No. 5965138  
GENERAL INFORMATION:  
APPLICANT: Cochran, Mark D  
APPLICANT: Junker, David  
APPLICANT: Wild, Martha A  
TITLE OF INVENTION: Recombinant Herpesvirus and Uses Thereof  
NUMBER OF SEQUENCES: 60  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: John P. White  
STREET: 1185 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/362,240A  
FILING DATE: Dec-22-94  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: White, John P  
REGISTRATION NUMBER: 28,678  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212)278-0400  
TELEFAX: (212)391-0526  
TELEX: 422523  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 577 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-362-240A-11

Query Match 97.4%; Score 2920; DB 2; Length 577;  
Best Local Similarity 96.9%; Pred. No. 5.1e-295;  
Matches 559; Conservative 8; Mismatches 10; Indels 0; Gaps 0;

QY 1 MDRAVSOVALNDEBEAKTWRLIFRIALLTVVTLATSVASLYSGASTPSDLVIGIP 60  
DB 1 MDRAVSOVALNDEBEAKTWRLIFRIALLTVVTLATSVASLYSGASTPSDLVIGIP 60  
QY 61 TRISRAEKITSTLGSNDQVVDRIYKQVLESPLALNTETTINMAITSLSYOINGANN 120  
DB 61 TRISRAEKITSTLGSNDQVVDRIYKQVLESPLALNTETTINMAITSLSYOINGANN 120  
QY 121 SGWAPRIHDPDPIGIGIKELIVDNASDVTSFYPSAFQEHNLFIAPPTGSGCTRIPSFDM 180  
DB 121 SGWAPRIHDPDPIGIGIKELIVDNASDVTSFYPSAFQEHNLFIAPPTGSGCTRIPSFDM 180  
QY 181 SATHYCYTHNVILSGCRDHS HQYLALGVLRRTATGRIFPSTLRSLDTONRKSCSV 240  
DB 181 SATHYCYTHNVILSGCRDHS HQYLALGVLRRTATGRIFPSTLRSLDTONRKSCSV 240  
QY 241 SATPLGCDMLCSKVTETEEEDYNSAVPTLMAHGRIGFDQGYHEKDLDTTLFGDWVANYP 300  
DB 241 SATPLGCDMLCSKVTETEEEDYNSAVPTLMAHGRIGFDQGYHEKDLDTTLFGDWVANYP 300  
QY 301 GVGGSFIDGWSVYSGGLKPNPSDPTVOGKVIYIRYNDTCDEDDYQIRAKKSYK 360  
DB 301 GVGGSFIDGWSVYSGGLKPNPSDPTVOGKVIYIRYNDTCDEDDYQIRAKKSYK 360  
QY 361 PGRFGKRIQQAIIISIKVSTSLGSDPVLTVPNTYTLGAGRIITVGTSHFLVORGSSY 420  
DB 361 PGRFGKRIQQAIIISIKVSTSLGSDPVLTVPNTYTLGAGRIITVGTSHFLVORGSSY 420  
QY 421 FSPALLYPMVSNKATILHSPYTFNAFTPGSIPCOASARCPNSCVTGVYTDPPYLLFYR 480  
DB 421 FSPALLYPMVSNKATILHSPYTFNAFTPGSIPCOASARCPNSCVTGVYTDPPYLLFYR 480

DB 421 FSPALLYPMVSNKATILHSPYTFNAFTPGSIPCOASARCPNSCVTGVYTDPPYLLFYR 480  
QY 481 NHTLRGVGTMLDSEQARLNPNASAVPSTSRIRTRVSSSSTKAYTSTCFKVKTKNT 540  
DB 481 NHTLRGVGTMLDSEQARLNPNASAVPSTSRIRTRVSSSSTKAYTSTCFKVKTKNT 540  
QY 541 YCLSIABISNTLFGFRIIVPLVEILKNDGVREARSG 577  
DB 541 YCLSIABISNTLFGFRIIVPLVEILKNDGVREARSG 577

RESULT 8  
US-08-480-640A-30  
Sequence 30, Application US/08480640A  
Patent No. 6033904  
GENERAL INFORMATION:  
APPLICANT: Cochran, Mark D.  
APPLICANT: Junker, David E.  
TITLE OF INVENTION: Recombinant Swinepox Virus  
NUMBER OF SEQUENCES: 225  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: John P. White  
STREET: 1185 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/480,640A  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: White, John P  
REGISTRATION NUMBER: 28,678  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 278-0400  
TELEFAX: (212) 391-0525  
INFORMATION FOR SEQ ID NO: 30:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 577 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-480-640A-30

Query Match 97.4%; Score 2920; DB 3; Length 577;  
Best Local Similarity 96.9%; Pred. No. 5.1e-295;  
Matches 559; Conservative 8; Mismatches 10; Indels 0; Gaps 0;

QY 1 MDRAVSOVALNDEBEAKTWRLIFRIALLTVVTLATSVASLYSGASTPSDLVIGIP 60  
DB 1 MDRAVSOVALNDEBEAKTWRLIFRIALLTVVTLATSVASLYSGASTPSDLVIGIP 60  
QY 61 TRISRAEKITSTLGSNDQVVDRIYKQVLESPLALNTETTINMAITSLSYOINGANN 120  
DB 61 TRISRAEKITSTLGSNDQVVDRIYKQVLESPLALNTETTINMAITSLSYOINGANN 120  
QY 121 SGWAPRIHDPDPIGIGIKELIVDNASDVTSFYPSAFQEHNLFIAPPTGSGCTRIPSFDM 180  
DB 121 SGWAPRIHDPDPIGIGIKELIVDNASDVTSFYPSAFQEHNLFIAPPTGSGCTRIPSFDM 180  
QY 181 SATHYCYTHNVILSGCRDHS HQYLALGVLRRTATGRIFPSTLRSLDTONRKSCSV 240  
DB 181 SATHYCYTHNVILSGCRDHS HQYLALGVLRRTATGRIFPSTLRSLDTONRKSCSV 240  
QY 241 SATPLGCDMLCSKVTETEEEDYNSAVPTLMAHGRIGFDQGYHEKDLDTTLFGDWVANYP 300  
DB 241 SATPLGCDMLCSKVTETEEEDYNSAVPTLMAHGRIGFDQGYHEKDLDTTLFGDWVANYP 300

QY 301 GVGGGSPIDRWFVSYYGGLKPNSPSDTVQEGKVIYKRYNDTCPEBQDYQIRMKSSYK 360  
DB 301 GVGGGSPIDRWFVSYYGGLKPNSPSDTVQEGKVIYKRYNDTCPEBQDYQIRMKSSYK 360  
QY 361 PGRFGGKRIQOAILSLKYSTSLGEBPVLTPPNTVTLMGAEGRIILVGTSHFLYORGSSY 420  
DB 361 PGRFGGKRIQOAILSLKYSTSLGEBPVLTPPNTVTLMGAEGRIILVGTSHFLYORGSSY 420  
QY 421 FSPALLYPMTVSNKRTATLHSPYTFNAFTPGSIPCOASARCPSCVTVGVTDPYPLIFR 480  
DB 421 FSPALLYPMTVSNKRTATLHSPYTFNAFTPGSIPCOASARCPSCVTVGVTDPYPLIFR 480  
QY 481 NHTLRGVFGTMDSEQARLNPASAVFDSRSRITRVSSSTKAAYTSTCFKVVTKNTK 540  
DB 481 NHTLRGVFGTMDSEQARLNPASAVFDSRSRITRVSSSTKAAYTSTCFKVVTKNTK 540  
QY 541 YCLISIAEISNTLFGERRIVPLVEILKNDGVREARSG 577  
DB 541 YCLISIAEISNTLFGERRIVPLVEILKNDGVREARSG 577

## RESULT 9

US-08-295-802-30  
; Sequence 30, Application US/08295802  
; Patent No. 6127163  
; GENERAL INFORMATION:  
; APPLICANT: Cochran Ph. D., Mark D  
; APPLICANT: Junker M.S., David E  
; TITLE OF INVENTION: Recombinant Swinepox Virus  
; NUMBER OF SEQUENCES: 188  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: John P. White  
; STREET: 30 Rockefeller Plaza  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10112  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; FILING DATE: Herewith  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: White, John P  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212)977-9550  
; TELEFAX: (212)664-0525  
; TELEX: 422523  
; INFORMATION FOR SEQ ID NO: 30:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 577 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-295-802-30

Query Match 97.4%; Score 2920; DB 3; Length 577;  
Best Local Similarity 96.9%; Pred. No. 5.1e-295;  
Matches 559; Conservative 8; Mismatches 10; Indels 0; Gaps 0;

QY 1 MDRAVSOVALENDEREAKNTWRLIFRIAILLTVTTLATSVASIVSMGASTPSDLVGP 60  
DB 1 MDRAVSOVALENDEREAKNTWRLIFRIAILLTVTTLATSVASIVSMGASTPSDLVGP 60  
QY 61 TRISRAEKTTSALGSQDYVDRIYKQVLAESPLALINTETITMAITSTSYOINGAANN 120  
DB 61 TRISRAEKTTSALGSQDYVDRIYKQVLAESPLALINTETITMAITSTSYOINGAANN 120

QY 121 SGWGAPIHDPDEFIGIGKELIVDNADVTSFYPSAFQEHNLNIPAPTTSGCTRIJPSFDM 180  
DB 121 SGWGAPIHDPDEFIGIGKELIVDNADVTSFYPSAFQEHNLNIPAPTTSGCTRIJPSFDM 180  
QY 181 SATHYCYTHNVILSGCRDSSHSHQYALGVLTATGRIFESTLNSISLDTQNRKSCSV 240  
DB 181 SATHYCYTHNVILSGCRDSSHSHQYALGVLTATGRIFESTLNSISLDTQNRKSCSV 240  
QY 241 SATPLGCDMLCSKVTETEEEDYNSAVPTLMAHGRIGFDCQYHEKLDVTTLPEDWVANY 300  
DB 241 SATPLGCDMLCSKVTETEEEDYNSAVPTLMAHGRIGFDCQYHEKLDVTTLPEDWVANY 300  
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DB 481 NHTLRGVFGTMDSEQARLNPASAVFDSRSRITRVSSSTKAAYTSTCFKVVTKNTK 540  
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DB 541 YCLISIAEISNTLFGERRIVPLVEILKNDGVREARSG 577

## RESULT 10

US-08-804-372A-9  
; Sequence 9, Application US/08804372A  
; Patent No. 6183753  
; GENERAL INFORMATION:  
; APPLICANT: Cochran, Mark D.  
; APPLICANT: Winslow, Barbara J.  
; TITLE OF INVENTION: Recombinant Chimeric Viruses and Uses  
; NUMBER OF SEQUENCES: 32  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Cooper & Dunham LLP  
; STREET: 1185 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10036  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; FILING DATE:  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: White, John P.  
; REGISTRATION NUMBER: 28,678  
; REFERENCE/DOCKET NUMBER: 2552/39115E  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 278-0400  
; TELEFAX: (212) 391-0525  
; INFORMATION FOR SEQ ID NO: 9:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 577 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein

US-08-804-372A-9

Query Match 97.4%; Score 2920; DB 3; Length 577;  
Best Local Similarity 96.9%; Pred. No. 5.1e-295;  
Matches 559; Conservative 8; Mismatches 10; Indels 0; Gaps 0;

QY 1 MDRVSOVALNDEBERAKNTWRLIFRIALLTLVTLATSVASLVYSGASTPSDLVGIP 60  
DB 1 MDRVSOVALNDEBERAKNTWRLIFRIALLTLVTLATSVASLVYSGASTPSDLVGIP 60  
QY 61 TRISAEKITSALGSNDVDRIYKQVLESPLALNTETTINMAITSLSYQINGANN 120  
DB 61 TRISAEKITSALGSNDVDRIYKQVLESPLALNTETTINMAITSLSYQINGANN 120  
QY 121 SGWGAIPHDPFICIGIKELIVDNASDVTSFYPSAFOEHLNFIAPPTGSGCTRIIPSDM 180  
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QY 181 SATHYCYTHNVILSGCRDHS HQYLALGVLRATSGVFTSLRSINLDDTQNRKSCSV 240  
DB 181 SATHYCYTHNVILSGCRDHS HQYLALGVLRATSGVFTSLRSINLDDTQNRKSCSV 240  
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DB 301 GVGGSFIDGRVWFSVYGLKPNPSDPTVOBGKVIYKRYNDTCPEBODYOIRMAKSSYK 360  
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DB 361 PGRFGKRIQOALISIKVSTSLGEDPVLTPPNTVTLMAEGRLITVGTSHFLYORSSY 420  
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DB 421 FSPALYPMVTVSNKTATLHSPYTFNAFTRPQSIPOQASARCPNSCVTVYTDYPPLIF 480  
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DB 481 NHTLRGVFTMLDSEORLNPASAVFDSSTSRITRVSSSTKAYTTSTCFKVKTKNT 540  
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DB 541 YCLSIASISNTLFGFRIVPLVLEILKNDGVEARSG 577

RESULT 11  
US-08-488-237A-30

; Sequence 30, Application US/08488237A  
; Patent No. 6251403  
; GENERAL INFORMATION:  
; APPLICANT: Cochran, Mark D.  
; APPLICANT: Junker, David E.  
; TITLE OF INVENTION: Recombinant Swinepox Virus  
; NUMBER OF SEQUENCES: 225  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: John P. White  
; STREET: 1185 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10036  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/488,237A  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:

; NAME: White, John P  
; REGISTRATION NUMBER: 28,678  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 278-0400  
; TELEFAX: (212) 391-0525  
; INFORMATION FOR SEQ ID NO: 30:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 577 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-488-237A-30

Query Match 97.4%; Score 2920; DB 3; Length 577;  
Best Local Similarity 96.9%; Pred. No. 5.1e-295;  
Matches 559; Conservative 8; Mismatches 10; Indels 0; Gaps 0;

QY 1 MDRVSOVALNDEBERAKNTWRLIFRIALLTLVTLATSVASLVYSGASTPSDLVGIP 60  
DB 1 MDRVSOVALNDEBERAKNTWRLIFRIALLTLVTLATSVASLVYSGASTPSDLVGIP 60  
QY 61 TRISAEKITSALGSNDVDRIYKQVLESPLALNTETTINMAITSLSYQINGANN 120  
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DB 121 SGWGAIPHDPFICIGIKELIVDNASDVTSFYPSAFOEHLNFIAPPTGSGCTRIIPSDM 180  
QY 181 SATHYCYTHNVILSGCRDHS HQYLALGVLRATSGVFTSLRSINLDDTQNRKSCSV 240  
DB 181 SATHYCYTHNVILSGCRDHS HQYLALGVLRATSGVFTSLRSINLDDTQNRKSCSV 240  
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DB 301 GVGGSFIDGRVWFSVYGLKPNPSDPTVOBGKVIYKRYNDTCPEBODYOIRMAKSSYK 360  
QY 361 PGRFGKRIQOALISIKVSTSLGEDPVLTPPNTVTLMAEGRLITVGTSHFLYORSSY 420  
DB 361 PGRFGKRIQOALISIKVSTSLGEDPVLTPPNTVTLMAEGRLITVGTSHFLYORSSY 420  
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DB 421 FSPALYPMVTVSNKTATLHSPYTFNAFTRPQSIPOQASARCPNSCVTVYTDYPPLIF 480  
QY 481 NHTLRGVFTMLDSEORLNPASAVFDSSTSRITRVSSSTKAYTTSTCFKVKTKNT 540  
DB 481 NHTLRGVFTMLDSEORLNPASAVFDSSTSRITRVSSSTKAYTTSTCFKVKTKNT 540  
QY 541 YCLSIASISNTLFGFRIVPLVLEILKNDGVEARSG 577  
DB 541 YCLSIASISNTLFGFRIVPLVLEILKNDGVEARSG 577

RESULT 12  
US-08-375-992A-30

; Sequence 30, Application US/08375992A  
; Patent No. 6328975  
; GENERAL INFORMATION:  
; APPLICANT: Cochran, Mark D.  
; APPLICANT: Junker, David E.  
; TITLE OF INVENTION: Recombinant Swinepox Virus  
; NUMBER OF SEQUENCES: 220  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: John P. White  
; STREET: 1185 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA



|||||  
Db 481 NHTLRGVGTMLDGEQARLNPASAVFDSSTSRITRVSSSIKAYTTSTCFKVKTKNT 540  
OY 541 YCLSIASISNTLFGFRIVPLVEILKNDGVEARSG 577  
Db 541 YCLSIASISNTLFGFRIVPLVEILKNDGVEARSG 577

## RESULT 14

PCT-US93-00324-30  
Sequence 30, Application PC/TUS9300324  
GENERAL INFORMATION:  
APPLICANT: Cochran Ph.D., Mark D  
APPLICANT: Junker M.S., David E  
TITLE OF INVENTION: Recombinant Swinepox Virus  
NUMBER OF SEQUENCES: 42  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: John P. White  
STREET: 30 Rockefeller Plaza  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10112  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US93/00324  
FILING DATE: 19930113  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: White, John P  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 977-9550  
TELEFAX: (212) 664-0525  
TELEX: 422523  
INFORMATION FOR SEQ ID NO: 30:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 577 amino acids  
TYPE: AMINO ACID  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
PCT-US93-00324-30

Query Match 97.4%; Score 2920; DB 5; Length 577;  
Best Local Similarity 96.9%; Pred. No. 5.1e-295;  
Matches 559; Conservative 8; Mismatches 10; Indels 0; Gaps 0;

OY 1 MDRAVSOVALENDREAKNTWRLIFRIAILLTAVTLATSVASLVYMGASTPSPDLVGP 60  
Db 1 MDRAVSOVALENDREAKNTWRLIFRIAILLTAVTLATSVASLVYMGASTPSPDLVGP 60  
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Db 61 TRIIRAEEKITSLAGSNODVDRIYKQVAVLESPLALNTETTINNAITSLSYQINGAAN 120  
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Db 121 SGWGAIPHDPFIGIGIKELIVDNASDVTSFYPSAFQEHNFIPAPTTGSGCTRIIPFDM 180  
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Db 181 SATHYCTHNVILSGCRDHS HQYLAAGVLRRTATGRIFSTLRSISLDTQNRKSCSV 240  
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Db 241 SATPLGCMILCSKYETEEDYNSAVPTIMAGRLGPDQYHEKLDVTTLFEEDVAVNY 300  
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OY 361 GPRFGKRIQOAILISIKVSTSLGSDPVLTPVNTVLMGAERILTVGTSHFLYQRGSSY 420  
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OY 541 YCLSIASISNTLFGFRIVPLVEILKNDGVEARSG 577  
Db 541 YCLSIASISNTLFGFRIVPLVEILKNDGVEARSG 577

## RESULT 15

PCT-US95-10245-11  
Sequence 11, Application PC/TUS9510245  
GENERAL INFORMATION:  
APPLICANT: SYNTRO CORPORATION  
TITLE OF INVENTION: Recombinant Herpesvirus of Turkeys And Uses Thereof  
NUMBER OF SEQUENCES: 60  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: John P. White  
STREET: 1185 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/10245  
FILING DATE: 09-AUG-1995  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: White, John P  
REGISTRATION NUMBER: 28,678  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 391-0526  
TELEFAX: (212) 391-0526  
TELEX: 422523  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 577 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
PCT-US95-10245-11

Query Match 97.4%; Score 2920; DB 5; Length 577;  
Best Local Similarity 96.9%; Pred. No. 5.1e-295;  
Matches 559; Conservative 8; Mismatches 10; Indels 0; Gaps 0;

OY 1 MDRAVSOVALENDREAKNTWRLIFRIAILLTAVTLATSVASLVYMGASTPSPDLVGP 60  
Db 1 MDRAVSOVALENDREAKNTWRLIFRIAILLTAVTLATSVASLVYMGASTPSPDLVGP 60  
OY 61 TRIIRAEEKITSLAGSNODVDRIYKQVAVLESPLALNTETTINNAITSLSYQINGAAN 120  
Db 61 TRIIRAEEKITSLAGSNODVDRIYKQVAVLESPLALNTETTINNAITSLSYQINGAAN 120  
OY 121 SGWGAIPHDPFIGIGIKELIVDNASDVTSFYPSAFQEHNFIPAPTTGSGCTRIIPFDM 180  
Db 121 SGWGAIPHDPFIGIGIKELIVDNASDVTSFYPSAFQEHNFIPAPTTGSGCTRIIPFDM 180  
OY 181 SATHYCTHNVILSGCRDHS HQYLAAGVLRRTATGRIFSTLRSISLDTQNRKSCSV 240  
Db 181 SATHYCTHNVILSGCRDHS HQYLAAGVLRRTATGRIFSTLRSISLDTQNRKSCSV 240

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Db 181 SATHYCYTHNVIIISGCRDHSHQYALGYLRTSATGRVFFSTLRSINLDDTONRKSCSV 240
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Db 241 SATPLGCDMLCSKYTEFEEDDYNASAVPTLMAHGRLGFDGOYHEKDLVTTLPEDWVANYP 300
QY 301 GVGGSFIDGRVWFSVYGLKPNSPSDTVQEGKVIYKRYNDTCPEQDYQIRMAKSSYK 360
Db 301 GVGGSFIDGRVWFSVYGLKPNSPSDTVQEGKVIYKRYNDTCPEQDYQIRMAKSSYK 360
QY 361 PGRFGGRRIQOAILISIVSTSLGEDPVLTVPNTVTLMGAEGRILTVGISHFLYORGSSY 420
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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

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2270.000 Million cell updates/sec

Title: US-09-915-515A-1

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Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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Published Applications AA:\*

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- 2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep:\*
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- 11: /cgn2\_6/ptodata/1/pubpaa/US09C\_PUBCOMB.pep:\*
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- 15: /cgn2\_6/ptodata/1/pubpaa/US10C\_PUBCOMB.pep:\*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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2	446	14.9	575	12	US-10-226-629A-17
3	145	4.8	1723	9	US-09-841-132-395
4	144	4.0	1723	9	US-09-841-132-394
5	119	4.0	1198	11	US-09-975-719-405
6	116	3.9	2283	12	US-10-172-502-4
7	114	3.8	5877	15	US-10-142-515-11
8	114	3.8	5935	15	US-10-243-243A-8
9	112.5	3.8	2344	9	US-09-815-242-12713
10	111	3.7	9799	12	US-09-965-738-146
11	111	3.7	11721	12	US-09-965-738-162
12	109.5	3.7	1510	10	US-09-738-626-3707
13	108	3.6	1609	10	US-10-369-493-1535
14	108	3.6	5636	12	US-10-033-189-128
15	108	3.6	5636	12	US-10-120-801-72

16	108	3.6	5636	12	US-10-023-634-93	Sequence 93, App1
17	106.5	3.6	1500	10	US-09-870-759-136	Sequence 136, App
18	106.5	3.6	1500	12	US-09-751-708A-136	Sequence 136, App
19	105.5	3.5	590	12	US-10-403-337-70	Sequence 70, App1
20	104.5	3.5	650	10	US-10-369-493-22177	Sequence 22177, A
21	104.5	3.5	689	15	US-10-202-846-2	Sequence 2, App11
22	104	3.5	1367	12	US-10-369-493-16732	Sequence 16732, A
23	102.5	3.4	1170	14	US-10-135-687-2	Sequence 2, App11
24	102.5	3.4	1210	10	US-09-660-352A-2	Sequence 2, App11
25	100.5	3.4	1752	12	US-10-387-388-2	Sequence 2, App11
26	100	3.3	345	10	US-09-738-626-6698	Sequence 6698, App
27	100	3.3	1316	12	US-10-028-248A-48	Sequence 48, App1
28	100	3.3	1797	12	US-10-369-493-5177	Sequence 5177, App
29	100	3.3	1805	12	US-10-369-493-5177	Sequence 5177, App
30	98	3.3	1160	12	US-10-115-482-46	Sequence 46, App1
31	98	3.3	1842	12	US-10-369-493-2225	Sequence 2225, App
32	97.5	3.3	834	12	US-10-094-749-2227	Sequence 2227, App
33	97.5	3.3	1082	12	US-10-369-493-17890	Sequence 17890, A
34	96.5	3.2	660	15	US-10-128-714-3291	Sequence 3291, App
35	96.5	3.2	794	15	US-10-128-714-8291	Sequence 8291, App
36	96.5	3.2	1659	10	US-09-801-368-118	Sequence 118, App
37	96	3.2	557	11	US-09-934-455-326	Sequence 326, App
38	96	3.2	557	12	US-10-302-267-198	Sequence 198, App
39	96	3.2	1075	12	US-09-801-368-110	Sequence 110, App
40	96	3.2	1075	12	US-10-369-493-22068	Sequence 22068, A
41	96	3.2	1110	15	US-10-149-819-12	Sequence 12, App1
42	96	3.2	1666	15	US-10-128-714-3553	Sequence 3553, App
43	96	3.2	1680	15	US-10-128-714-8553	Sequence 8553, App
44	96	3.2	1751	9	US-09-841-132-445	Sequence 445, App
45	96	3.2	1751	9	US-09-841-132-594	Sequence 594, App

#### ALIGNMENTS

RESULT 1  
US-09-915-515A-1  
; Sequence 1, Application US/0915515A  
; Patent No. US20020081572A1  
; GENERAL INFORMATION:  
; APPLICANT: Taylor, Gary  
; APPLICANT: Portner, Allen  
; APPLICANT: Takimoto, Toru  
; APPLICANT: Babu, Y. Sudhakar  
; APPLICANT: Rowland, R. Scott  
; TITLE OF INVENTION: three Dimensional Structure of Paramyxovirus Hemagglutinin-Neurami  
; FILE REFERENCE: 1663/00142  
; CURRENT APPLICATION NUMBER: US/09/915, 515A  
; CURRENT FILING DATE: 2001-12-18  
; NUMBER OF SEQ ID NOS: 1  
; SEQ ID NO 1  
; LENGTH: 577  
; TYPE: PRT  
; ORGANISM: Newcastle Disease Virus (Kansas Strain)  
US-09-915-515A-1

Query Match 100.0%; Score 2998; DB 9; Length 577;  
Best Local Similarity 100.0%; Pred. No. 7e-289;  
Matches 577; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MDRAVSVQVLENDREANKNTWRLIFRIAILLLTVTLATSVASLVYSGASTPDIIVIP	60
DB	1	MDRAVSVQVLENDREANKNTWRLIFRIAILLLTVTLATSVASLVYSGASTPDIIVIP	60
QY	61	TRISRAEKITSALGSNDVDRIRYKOVLESPLALNTETITNNATISLSYQINGANN	120
DB	61	TRISRAEKITSALGSNDVDRIRYKOVLESPLALNTETITNNATISLSYQINGANN	120
QY	121	SGKAPIHDPPIFGIGIKELIVDNASDVTSFYPSAFQSHLNFIPAPTTGSGCTRIIPSDM	180
DB	121	SGKAPIHDPPIFGIGIKELIVDNASDVTSFYPSAFQSHLNFIPAPTTGSGCTRIIPSDM	180

QY	181	SATYCYTHANVILSGCRRHSHSHOYLAVGLRTATGIFPSTLRSLSDDTQRRKCSV	240
Db	181	SATHYCTHANVILSGCRRHSHSHOYLAVGLRTATGIFPSTLRSLSDDTQRRKCSV	240
QY	241	SATPLGCDMLCSKYTETEEDDYNASVPTLMAHGRIGFDQYHEKDLVYTLFEDMVANYP	300
Db	241	SATPLGCDMLCSKYTETEEDDYNASVPTLMAHGRIGFDQYHEKDLVYTLFEDMVANYP	300
QY	301	GVGGGSLFDGWNSSVYGLKPNBPSDTVOGKVIYIKRYNDTCPEDEDYQIRMAKSSYK	360
Db	301	GVGGGSLFDGWNSSVYGLKPNBPSDTVOGKVIYIKRYNDTCPEDEDYQIRMAKSSYK	360
QY	361	PGRGGRIRIOAIIISIKVSTSLGEDPVLTVPEPNTWTLMGAEGRLITVGTSHFLYQRGSSY	420
Db	361	PGRGGRIRIOAIIISIKVSTSLGEDPVLTVPEPNTWTLMGAEGRLITVGTSHFLYQRGSSY	420
QY	421	FSPALLVPMYTSNKTATILHSPYTFNAFTRPGSIPCOASARCPNCSVGVYDVPPLIFYR	480
Db	421	FSPALLVPMYTSNKTATILHSPYTFNAFTRPGSIPCOASARCPNCSVGVYDVPPLIFYR	480
QY	481	NHTLRGVFGTMLDSEQARLNPASAVFDSSTSSRITRVSSTSKAAYTTSTCFKXVKTNKT	540
Db	481	NHTLRGVFGTMLDSEQARLNPASAVFDSSTSSRITRVSSTSKAAYTTSTCFKXVKTNKT	540
QY	541	YCLSIARESNTLPGEPFRIVPLVLEILKNDGVRERASG	577
Db	541	YCLSIARESNTLPGEPFRIVPLVLEILKNDGVRERASG	577

```

RESULT 2
US-10-226-629A-17
Sequence 17, Application US/10226629A
Publication No. US20030166504A1
GENERAL INFORMATION:
APPLICANT: Myriad Genetics, Inc.
APPLICANT: Morham, Scott
APPLICANT: Zavit, Kenton
APPLICANT: Hobden, Adrian
TITLE OF INVENTION: Therapeutic Compositions and Methods for Treating Viral Infection
FILE REFERENCE: 5006.01
CURRENT APPLICATION NUMBER: US/10/226, 629A
CURRENT FILING DATE: 2002-08-22
PRIOR APPLICATION NUMBER: US 60/314,182
PRIOR FILING DATE: 2001-08-22
NUMBER OF SEQ ID NOS: 736
SOFTWARE: PatentIn version 3.1
SEQ ID NO 17
LENGTH: 575
TYPE: PRT
ORGANISM: Human parainfluenza virus 1
US-10-226-629A-17

Query March 14.9%; Score 446; DB 12; Length 575;
Best local similarity 27.5%; Pred. No. 5.2e-35;
Matches 155; Conservative 92; Mismatches 237; Indels 80; Gaps 20;

QY 26 RIALLLIVTVTLATSV-----SLVYSNGASTPSDLVGIPTRISRA--EEKITSAL 74
||| ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 32 RIHMLIATMTHTVLSFTIMILICIDILIKODTCMKITMTVMSMNESAKTIKETITELI 91
||| ||| : : : : : : : : : : : : : : : : : : : : : : : : :

QY 75 GSNDDVDR-LYKQVALESP-ALLNTEETIMNAITLSVYINGAANNSGCAPIHPDPF 132
||| ||| : : : : : : : : : : : : : : : : : : : : : : : : :
Db 92 --ROEVISRTININOSVOSGIPILINKOSRDLTQIIEKSCRQELAQICENTAIHHADG 149
||| ||| : : : : : : : : : : : : : : : : : : : : : : : : :

QY 133 IG-----GIGKELIVDNASDVTSFPYSAFOEHLNFIAP-----TTGSGCTRIP 176
||| ||| : : : : : : : : : : : : : : : : : : : : : : : : :
Db 150 ISPLDPHDFMRCAPGEPLLSNN-----PNISLLPGBSLLSGSTTISGCVRLP 196
||| ||| : : : : : : : : : : : : : : : : : : : : : : : : :

QY 177 SFDMSATHYCYTHAVILVSGCPDHSHOYLAVGLRTTATGRIFFSTLRSLSDLTQNRK 236
||| ||| : : : : : : : : : : : : : : : : : : : : : : : : :
Db 197 SLISGDALIVASSNLITQGCADICKSTOVOLGYSILNSDMYPDLNPIVISHTYINDNRK 256
||| ||| : : : : : : : : : : : : : : : : : : : : : : : : :

QY 237 SCSVSATPLGCDMLCSKVTETEEDDYNSAVPTLMAHGRLGFDG-----QYHEKDLDVTTL 291
||| ||| : : : : : : : : : : : : : : : : : : : : : : : : :

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[illegible]

```

RESULT 3
US-09-841-132-395
: Sequence 395, Application US/09841132
: Patent No. US20020061848A1
GENERAL INFORMATION:
APPLICANT: Bhalla, Ajay
APPLICANT: Skelky, Yahir A.W.
APPLICANT: Probst, Peter
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
: TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
FILE REFERENCE: 210121.469C8
CURRENT APPLICATION NUMBER: US/09/841.132
CURRENT FILING DATE: 2001-04-23
NUMBER OF SEQ ID NOS: 599
SOFTWARE: FastSeq for Windows Version 3.0/4.0
SEQ ID NO 395
LENGTH: 1723
TYPE: PRT
ORGANISM: Chlamydia pneumoniae
US-09-841-132-395

```

Query Match	4.8%	Score 145;	DB 9;	Length 1723;
Best Local Similarity	18.8%	Pred. No. 0.00028;		
Matches 141;	Conservative 88;	Mismatches 284;	Indels 236;	Gaps 239

  

Qy	4	AVSOVALEN--DEREAKTWR-----	-LIFRIAILLTVTVLATSVASLVYSMG	49
Db	449	AVGQVLTLEDIAALKMTNTCKGEGAIYTKALKLTINNGALLTTPSGTSTIDNGCALFVAG	508	
Qy	50	ASTPSDLVGI---PRISRAEKKITSALGNOQVDVRIYQVALESPL-----	94	
Db	509	GITLSDLVEVRFSKKKTGNYAPAPIKAASNPAPVVS--SSTTAASEPVAAPAAAAPVTA	565	
Qy	95	-----ALNLTETINNAITSLSYQINGANNNGMWAPI-----	-HDPDFI-----	133
Db	566	AKGALAYSTEGTLVAGITSLISFENNECQNGGAYVTKTPQCSDSHRLQFTSNKAADG	625	
Qy	134	GGI--GKEILIVNADSVTSFYPSAPFOEH-----	-LNFIAPETTG	170
Db	626	GGLYCGDDVTLTNLTKGLTFQENSEKRGGSLASLAKSLTMTSLBFCINATAENG	685	
Qy	171	GCTRIPSPFMSATHCYTHNVILSGCRDHS--	-----QYALGVLRFTTAGRI	220
Db	686	G-ANVP-----	ENIVLFTPTYPTEBPAVQGPVYGALVTGNTATKSGGIY	732
Qy	221	-----FSTIRSLSDDTQNRKSCSVATPLCCDMLCSKRTETEDEDYNSAVPLIMAHGR	275	
Db	733	TKMAAFNSNLSTYFPQNTSSENGALLTQKAAKTDCSPFYITVNVLTNNNTAANGGGIA	792	



276 GFDGQYHEKDLDTTLFEDWVANYPGVGGSFIDGRVWF--VYGLKPNSPDPTGOK 333  
Db 793 G--GKAHFDRIIDLTV-----OSNOAKKGCGVYLEDALILEKVITGVSQN---TATESG 842  
Qy 334 VYIKRYNDTPDEDDYQIRMAKSSYKPRGGRIOQALISIKVSTSLGEDPVL---T 389  
Db 843 GGITAK-----DIQLOAL-----PGSF-----TTIDNKVETSLLTSTNLVGGGI 881  
Qy 390 VPPVTVTLMAEG-----RIITVGTSHFLYORSSYFSPALLPYMTVSNKKTATLHSPY 442  
Db 882 YSSGAVTLTNSIGTFGTGNSVINTATISODADIOGGIYA-----TTSLSINOCNTP 934  
Qy 443 TF--NAFTRPGSIPCGASARCPNSCVTYTDPYPLIFRNH-----GTMDSQARL 482  
Db 935 LFSNNSATKKTSTTKQIAGGAIPSAVTIENNSQPIIFLNNSAKSEATTAATAGNKDSC 994  
Qy 483 -----TLRGVF-----GTMDSQARL 499  
Db 995 GGAIAANSVTLTNPEITFGNVAETGAIGCIDLTNGSPPRKVSADNGSVLFOQNSAL 1054  
Qy 500 NPASAVFDSST--SRSRITRVSSSTK--AAVTTSTCF-----KVYKTKNTY 541  
Db 1055 NRGAIYGETIDIRTGATPIFGNSKHDGSAICCTALTAPNSQLFENNKVETTTATT 1114  
Qy 542 CLSIAEISNTLFGERRIVPLVLEIKNDG 570  
Db 1115 KASINNLGAALYGNNETSDVITISLAENG 1143

RESULT 4  
US-09-841-132-394  
Sequence 394, Application US/09841132  
Patent No. US20020061848A1  
GENERAL INFORMATION:

APPLICANT: Bhactia, Ajay  
APPLICANT: Skeiky, Yasir A.W.  
APPLICANT: Probst, Peter  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND  
FILE REFERENCE: 210121.469C8  
CURRENT APPLICATION NUMBER: US/09/841.132  
CURRENT FILING DATE: 2001-04-23  
NUMBER OF SEQ ID NOS: 599  
SOFTWARE: FastSeq for Windows Version 3.0/4.0  
SEQ ID NO 394  
LENGTH: 1723  
TYPE: PRT  
ORGANISM: Chlamydia pneumoniae  
US-09-841-132-394

Query Match 4.8%; Score 144; DB 9; Length 1723;  
Best Local Similarity 18.8%; Pred. No. 0.00035;  
Matches 141; Conservative 88; Mismatches 284; Indels 236; Gaps 29;  
Qy 4 AVSOVALEN--DEREAKNTWR-----LIFRAIILLTVTLATSVASLVSMG 49  
Db 449 AVGOVTLLEDIANLKMNTNCKGEGAIYTKALITNNAILTTSGNSTNGCAIFAVG 508  
Qy 50 ASTPSDLVGT--PRTSRABEKITSALGNSODVYDRIYKOVALESPI-----94  
Db 509 GITLSDLEVEFRSKKTKGNSAPITKASNTAPVVS--SSTTAASPAVPAAPAAAPVNA 565  
Qy 95 -----ALNTEETINMAITSLSYOINGAANNNGMGAPI-----HDPDI-----133  
Db 566 AKGALISTBGLTVSGITSLISFENNECONOGGAYVTKTQCSDSHRLQFTSNKADEG 625  
Qy 134 GGI--GKELIVDNASDVTSFYPSAFOEH-----LNFIPAPTTGS 170  
Db 626 GGIVCGDGVTLTNLTKTLFQENSEKRGKGGSLASGSLMTSLESFCLANANTAKENG 685  
Qy 171 GCTRIPSDMSATHYCYHNAILSGCRDHS--OYALGVLTATTATGRIF 220  
Db 686 G-ANVP-----ENIVLFTYPTTNEPAPVQPVYGEALVYGNATATYSGGGIY 732

221 -----FSTLSISIDPTONRKSCSVSATPLGCDMLCSKETEEDYNSAVPTLMAHRL 275  
Db 733 TKNAFENLSVTDQNTSSNGGALLTQKRAADTDGSEFTYITVNTLNNTATNGGGIA 792  
Qy 276 GFDGQYHEKDLDTTLFEDWVANYPGVGGSFIDGRVWF--VYGLKPNSPDPTGOK 333  
Db 793 G--GKAHFDRIIDLTV-----OSNOAKKGCGVYLEDALILEKVITGVSQN---TATESG 842  
Qy 334 VYIKRYNDTPDEDDYQIRMAKSSYKPRGGRIOQALISIKVSTSLGEDPVL---T 389  
Db 843 GGITAK-----DIQLOAL-----PGSF-----TTIDNKVETSLLTSTNLVGGGI 881  
Qy 390 VPPVTVTLMAEG-----RIITVGTSHFLYORSSYFSPALLPYMTVSNKKTATLHSPY 442  
Db 882 YSSGAVTLTNSIGTFGTGNSVINTATISODADIOGGIYA-----TTSLSINOCNTP 934  
Qy 443 TF--NAFTRPGSIPCGASARCPNSCVTYTDPYPLIFRNH-----GTMDSQARL 482  
Db 935 LFSNNSATKKTSTTKQIAGGAIPSAVTIENNSQPIIFLNNSAKSEATTAATAGNKDSC 994  
Qy 483 -----TLRGVF-----GTMDSQARL 499  
Db 995 GGAIAANSVTLTNPEITFGNVAETGAIGCIDLTNGSPPRKVSADNGSVLFOQNSAL 1054  
Qy 500 NPASAVFDSST--SRSRITRVSSSTK--AAVTTSTCF-----KVYKTKNTY 541  
Db 1055 NRGAIYGETIDIRTGATPIFGNSKHDGSAICCTALTAPNSQLFENNKVETTTATT 1114  
Qy 542 CLSIAEISNTLFGERRIVPLVLEIKNDG 570  
Db 1115 KASINNLGAALYGNNETSDVITISLAENG 1143

RESULT 5  
US-09-975-719-405  
Sequence 405, Application US/09975719  
Publication No. US20030022349A1  
GENERAL INFORMATION:

APPLICANT: Ausubel, Frederick M.  
APPLICANT: Rahme, Laurence G.  
TITLE OF INVENTION: VIRULENCE-ASSOCIATED NUCLEIC ACID  
FILE REFERENCE: 00786/361003  
CURRENT APPLICATION NUMBER: US/09/975.719  
CURRENT FILING DATE: 2001-10-10  
PRIOR APPLICATION NUMBER: US 09/199,637  
PRIOR FILING DATE: 1998-11-25  
PRIOR APPLICATION NUMBER: US 60/066,517  
PRIOR FILING DATE: 1997-11-25  
NUMBER OF SEQ ID NOS: 437  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 405  
LENGTH: 1198  
TYPE: PRT  
ORGANISM: Pseudomonas aeruginosa  
US-09-975-719-405

Query Match 4.0%; Score 119; DB 11; Length 1198;  
Best Local Similarity 21.3%; Pred. No. 0.06;  
Matches 83; Conservative 53; Mismatches 112; Indels 142; Gaps 21;  
Qy 59 IPT-----RIRAREKITSALGNSODV--DRIYQVAL--ESPALNTEETIM 105  
Db 33 IPTWQORMHQITRAKSLIAA-GCTLSTLIFASDSYAATLAVNSQOPFLV--TQVAPN 89  
Qy 106 AITSL-----SYOINGAANNNG-----WCAPLHDPDFIGIGKELIVDNASDVTS 150  
Db 90 LILFLUDSGSMAAYVVDGIGSNGSGRAGRSDDVYALVYNDYAYQVKKLTLSDQIIVS 149  
Qy 151 FYP-----SAFOEHL-----NFIAPPTG--SGC-----TRIP 176  
Db 150 DYPVPRFAAMQDVGAGSTTNLSNNYRPMQGTGMLCIDSSCNTGRAYVYTVKVASACP 209



Db 1246 SIFGP-----AOSTMSLIDSEVYTRLSTSPIMESAEITTTTQGYSLATSQVTLPLG 1299  
Qy 394 T-VTLGAGEGRILTVGTSHF-----LYORGS---SYFSPALL-----YPMT---VS 432  
Db 1300 TSMFTLSGSHGTHMGQGLSHSEMTLMRGPSLSMTSPRFETRRSSSLSLTLTSLLS 1359  
Qy 433 NKTATL-----HSPYTFNAFTRP-----SIPCOASARCPNSCTGVYTDPPYL 476  
Db 1360 PVSSTLIDSSPSSPLPVTSLLPLGLVKTEVLDTSSEPKTSS--PNLSSTSV----- 1410  
Qy 477 IFYRNHTLRGVFGTMDLSEQ-----ARLNPAASAVFDS-----TSRRTIRVSSSS 521  
Db 1411 -----EIPATSEIMTDEKIHPSSENTAVAKVRTSSVHSHSVLADSETTTITPMSGI 1464  
Qy 522 TKA-----AYTSTGCF---KVYKTKNTYCL-----SIAISNTLFG 554  
Db 1465 TSAVEDTTFVTSNPAFSETRRIPTEPTFSLTPGPRETSTSEETTSITETSAVLFG 1519

RESULT 8  
US-10-243-243A-8

Sequence 8, Application US/10243243A  
Publication No. US2003010442A1  
GENERAL INFORMATION:  
APPLICANT: Lleyd, Kenneth O.  
APPLICANT: Yin, Beatrice W.T.  
TITLE OF INVENTION: Nucleic Acid Sequence Encoding Ovarian Antigen, CA125, and Uses T  
FILE REFERENCE: 649-B  
CURRENT APPLICATION NUMBER: US/10/243,243A  
PRIOR FILING DATE: 2002-09-19  
PRIOR APPLICATION NUMBER: US 10/142,515  
PRIOR FILING DATE: 2002-05-09  
PRIOR APPLICATION NUMBER: PCT/US02/14768  
PRIOR FILING DATE: 2002-05-09  
PRIOR APPLICATION NUMBER: US 60/290,480  
NUMBER OF SEQ ID NOS: 10  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 8  
LENGTH: 5935  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: MISC FEATURE  
LOCATION: (1) (5935)  
OTHER INFORMATION: Amino acid sequence of MUC16B  
US-10-243A-8

Query Match 3.8%; Score 114; DB 15; Length 5935;  
Best Local Similarity 19.7%; Pred. No. 2.6;

Matches 141; Conservative 96; Mismatches 236; Indels 242; Gaps 35;

Qy 28 ALLTLTVTLATSVASLVYSMG-----ASTP--SDLVGIPTRISPAEKITSAL---GSN 77  
Db 930 SVLADSVTTKATSSMGITPTGDTNVLSTPAFSOTSIQT---KXSLRPLGLMETSLIS 986  
Qy 78 ODVVDRIKQVALBEPPLALNTEITIMATISLSQINGAANSGWAPHDPTGIGIG 137  
Db 987 EETSSATEKSTVLSVPTGATTEVSRTAISSSRTSISIGPPOST-----MS 1032  
Qy 138 KELIYDNASDVTSFPAFAFOEHLNFIAPPTG--SGCTRIPSFDM-----SATH 184  
Db 1033 SDTSMETTRIST--PLTRKESTDAITPKTGPSGATSGGFTTLSSSTASMPGTHSAT 1090  
Qy 185 YCYTHNVILS-----GCRDHS-----HSHOYLAGVLRRTATG----- 217  
Db 1091 QRFPRSVVTTTPMSRGPEDEVMPSPLSVEKNPSPPSLVSSSVTSPPSYSTPSGSHSP 1150  
Qy 218 -----RIFSTLARSIS--LDDTONRKSQSVSATPLGCD--MLCSKYTEEBEDYNSAVPTL 269  
Db 1151 VPTVSLTSLTSLIMKATMDLADSLSEPTTSAPNNNTISDESLSASKAT--TETEAHVFEENTA 1209

Qy 270 MAHGRIGFGQYHEKDLDTVTLFEDVWVANYPG-----VGGGSFLIDGRVWFPSVG 318  
Db 1210 ASH-----VETTSATELELVSSSPGFSEPTKVISPVVTSSIRNNWVSTTMPG 1256  
Qy 319 -----GLKPNSPDVT---QBEKVYIYKRYNDTCPEBODYQIRMAKS 358  
Db 1257 SSGITRIEISMSSLTFLGLRETRISODITSTSTSTVLYKMPGATPEVRSFVMPSSRT 1316  
Qy 359 YKPRFGGRKIQOALISIKVS-----TSIGEDPVV-----TYPNN 393  
Db 1317 SIFGP-----AOSTMSLIDSEVYTRLSTSPIMESAEITTTTQGYSLATSQVTLPLG 1370  
Qy 394 T-VTLGAGEGRILTVGTSHF-----LYORGS---SYFSPALL-----YPMT---VS 432  
Db 1371 TSMFTLSGSHGTHMGQGLSHSEMTLMRGPSLSMTSPRFETRRSSSLSLTLTSLLS 1430  
Qy 433 NKTATL-----HSPYTFNAFTRP-----SIPCOASARCPNSCTGVYTDPPYL 476  
Db 1431 PVSSTLIDSSPSSPLPVTSLLPLGLVKTEVLDTSSEPKTSS--PNLSSTSV----- 1481  
Qy 477 IFYRNHTLRGVFGTMDLSEQ-----ARLNPAASAVFDS-----TSRRTIRVSSSS 521  
Db 1482 -----EIPATSEIMTDEKIHPSSENTAVAKVRTSSVHSHSVLADSETTTITPMSGI 1535  
Qy 522 TKA-----AYTSTGCF---KVYKTKNTYCL-----SIAISNTLFG 554  
Db 1536 TSAVEDTTFVTSNPAFSETRRIPTEPTFSLTPGPRETSTSEETTSITETSAVLFG 1590

RESULT 9  
US-09-815-242-12713

Sequence 12713, Application US/09815242  
Patent No. US20020061569A1  
GENERAL INFORMATION:  
APPLICANT: Haselbeck, Robert  
APPLICANT: Ohlsen, Kari L.  
APPLICANT: Zykend, Judith W.  
APPLICANT: Wall, Daniel  
APPLICANT: Trawick, John D.  
APPLICANT: Carr, Grant J.  
APPLICANT: Yamamoto, Robert T.  
TITLE OF INVENTION: Identification of Essential Genes in  
FILE REFERENCE: EUTRA-011A  
CURRENT APPLICATION NUMBER: US/09/815,242  
PRIOR FILING DATE: 2001-03-21  
PRIOR APPLICATION NUMBER: 60/191,078  
PRIOR FILING DATE: 2000-03-21  
PRIOR APPLICATION NUMBER: 60/206,848  
PRIOR FILING DATE: 2000-05-23  
PRIOR APPLICATION NUMBER: 60/207,727  
PRIOR FILING DATE: 2000-05-26  
PRIOR APPLICATION NUMBER: 60/242,578  
PRIOR FILING DATE: 2000-10-23  
PRIOR APPLICATION NUMBER: 60/253,625  
PRIOR FILING DATE: 2000-11-27  
PRIOR APPLICATION NUMBER: 60/257,931  
PRIOR FILING DATE: 2000-12-22  
PRIOR APPLICATION NUMBER: 60/269,308  
PRIOR FILING DATE: 2001-02-16  
NUMBER OF SEQ ID NOS: 14110  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 12713  
LENGTH: 2344  
TYPE: PRT  
ORGANISM: Staphylococcus aureus  
US-09-815-242-12713

Query Match 3.8%; Score 112.5; DB 9; Length 2344;  
Best Local Similarity 18.9%; Pred. No. 0.8;  
Matches 125; Conservative 89; Mismatches 251; Indels 195; Gaps 24;

```
QY 33 TTVTLATSVAS-LVYSGASTPSDLVGIPTIRISAEKITSALGSN-----DVIDR 83
Db 606 TTVNTVTGLSGSLD---SATNSIIIGTPKIGGSTVTVSTDQANKSTTTFTINVDI 662
QY 84 IY-----KQVLESPPLALLNET-----TITMAITSLISYOIN-GAANNCGMGPPIH 128
Db 663 TAPVTPIGDKSSSEVFSPISPINATQDNGNAVTVTGLPQGLTPDSTNNNTISGPTN 722
QY 129 DDPDGGIGKELELYVDNADVTSPFSAFOEHLNIPAPVTGSGGCTRI.PSFDMAITHYCYT 188
Db 723 -----IGSTITIVSTD-----ASGNKTTTTRKEYTIRNSMS 754
QY 189 HNVILSGCRSHSHS-----HOYALGVLRATATGRI.PFSTLRSLDLDTQNRKSCSVS 241
Db 755 DSVGTSSTQOQSGSVTSKADSGAS-----TSTSGIMTSTAITS-----KSTSVS 802
QY 242 ATPGCMGLCSKYETEED-YNSAVPTLMAHGLGDQGHEDDVTTLFEDMVAN-- 238
Db 803 ---LSDSVASAKSLISTESNSVSSSTSTSLVNSQSVSSM--SGSVKSTSLSDPISNSG 857
QY 299 -----YPGVGGGFIDGRVWFVSVYGLKPN-----SPSDTVQSGKYVIYKRYN 341
Db 858 STEKSESVSTSTSLSTSLSDSVSMSTSGLSKQSLSTSTSDASTSGSVSDSTN 917
QY 342 DTCPDEQ-----DYQIRMAKSSYKPRGKRIQOAILSIKYSTS-----381
Db 918 SISTRSELSBSGTSSEISISINSVSASTSKLESQSTISLSTDSKMSSTSESLD 977
QY 382 -----LEGDPVLTVPPNTV-----TIMGABGILLVYGTSHFL 413
Db 978 STSTSDSVSGSLSVAGSQSVSTSTSDMSSTSEMISDMSSTGSLAASDSKMSVSSMSST 1037
QY 414 YORGSYFSPALLYPMVTVSNKTATLHSPYENAFTRPGSIPCOASARCPNSCVTVGYTDP 473
Db 1038 SQSGST--SESLASISTSDSGSKSLSTSGSGSTSTSTSTSSVMSSESOSTS-----1090
QY 474 YPLIFYENHTLRGVFGTMDSEQARLNPAASAVPDSRSR-----ITRVSSSGTKA 524
Db 1091 -----GSMSTSGSDSTSTSTSTSTSTSDSKASATPASESISQSVSTSG 1135
QY 525 AYTSTSTCFKVVYKNTK-----YCLSIATISNTLFGEFRIVPLVILKNDGVREARSG 577
Db 1136 SVSTSTSLSTNSERTSTSMDSSTSLSTSESDST-----SDSTSTSDISEAISG 1185

RESULT 10
US-09-965-738-146
; Sequence 146, Application US/09965738
; Publication No. US20030143667A1
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy
; TITLE OF INVENTION: Repeat Sequences of the CA125 Gene and Their Use for Diagnostic
; FILE REFERENCE: 40715-258841
; CURRENT APPLICATION NUMBER: US/09/965,738
; PRIOR FILING DATE: 2001-09-27
; PRIOR APPLICATION NUMBER: US 60/284,175
; NUMBER OF SEQ ID NOS: 306
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 146
; LENGTH: 9799
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)..(9799)
; OTHER INFORMATION: Any "X" = any amino acid
US-09-965-738-146

Query Match 3.7%; Score 111; DB 12; Length 9799;
Best Local Similarity 19.8%; Pred. No. 12;
Matches 117; Conservative 76; Mismatches 198; Indels 200; Gaps 28;
```

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QY 31 LITVTLATSVASLVYSGASTPSDLVGIPTIRISAEKITSALGS---NODVDRIVYQ 87
Db 1254 LVPFTLNTLTINLQGEEDMHRP-----SRKNATERVLQGLSPIRKSSVGLVYSG 1307
QY 88 VALSEPPLALLNETTITMAITSLISYOINCAANNCGMGPIDDPDGGIGKELELYDNASD 147
Db 1308 CRL-----TSLRPEKDGAAATGMDAVCLYHNPCKRPGLDREQLYEWELQ 1350
QY 148 VT-----SFYPSAQEHLNIPFA-----PTTGS-----GC 172
Db 1351 LTNITELGPYSLDRDSLTVNGP--THQNSVPTTSPGISTVYWTATGTPSSFPGHTEPGR 1409
QY 173 TRIP-SFDMASATHYCYTHNVILSGCRDSSHQYALAVL-----RTATGRIFFSTLRGI 227
Db 1410 LLIPTFNFTLINHAEEMQHPSKXFTTERVLQ-GILKPLFNKTSVGPL-YSGCRLT 1467
QY 228 SLDDTQ-----NRKCSVASATPLGCDM--LCSKVETEEDYNSAVPTLM 270
Db 1468 SLRPEKDGAAATGMDAVCLYHNPCKRPGLDREQLYCELQTLTNITELG-----PYSL 1519
QY 271 AHGRIGFDQGYHEKQDVTTLFEDMVANYPGVGGGFFIDGRVWFVSVYGLKPNPSDITQ 330
Db 1520 DRDSLTVNGPFTHONSVPITST-----PGT-----STVYMATG--TSSSPGHTE 1562
QY 331 ECKYVIYKRYNDTCPEDEQDYQIRMAKSSYKPG--RFG-GKRIQOAILIS-IKYSTSLGE-- 384
Db 1563 PGLPLIFPTFNFTLIN-----LHYEENMQHPSRKNTTERVLQGLKPLFNKTSVGPLY 1617
QY 385 -----DPV-----LYVPPNVTLMGAEGRLL 405
Db 1618 SGCRLLTLRPEKHEATGVDTICTHRVDPICGLDRERLYWELSQLTNSITELGP-----1672
QY 406 TVGTSHFLQRGSSY--RSPALVPMVTVSNKTATLHSPYENAFTRPGSIPCOASARCP 462
Db 1673 -----YTLDRDSLTVNGFPNPSVPTTSPGISTVHLATSGTSSLPG-----1715
QY 463 NSCVTVGYTDPYPLI--FYRNHTLRGVFGTMDSEQARLNPAASAVPDSRSR 511
Db 1716 -----HTAPVPLIPLFTLNFTI-----TNLHYEENMQHPSRKNTTER 1754

RESULT 11
US-09-965-738-162
; Sequence 162, Application US/09965738
; Publication No. US20030143667A1
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy
; TITLE OF INVENTION: Repeat Sequences of the CA125 Gene and Their Use for Diagnostic
; FILE REFERENCE: 40715-258841
; CURRENT APPLICATION NUMBER: US/09/965,738
; PRIOR FILING DATE: 2001-09-27
; PRIOR APPLICATION NUMBER: US 60/284,175
; NUMBER OF SEQ ID NOS: 306
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 162
; LENGTH: 11721
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)..(11721)
; OTHER INFORMATION: any x = any amino acid
US-09-965-738-162

Query Match 3.7%; Score 111; DB 12; Length 11721;
Best Local Similarity 19.8%; Pred. No. 16;
Matches 117; Conservative 76; Mismatches 198; Indels 200; Gaps 28;
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```

Db 2892 LVPFTLNTLNQYEDMARG-----SRKNATERVLOGLSPFKNSVGPYSG 2945
Qy 88 VALSEPLALNTETTMAITSLSYOINGAANNNGMGAIPHDPFGIGKELIYDNASD 147
Db 2946 CRL-----TSLRPEKDAATGMADVCLYHNPKRPGIDRQGLWELSQ 2988
Qy 148 VT-----SFPASFOEHLNFIPIA-----PTTGS-----GC 172
Db 2989 LTHNITELGPYSLDRDSLIVNGF-THONSVPPTSTPGSTVYMAATGPPSPGHTBGP 3047
Qy 173 TRIP-SFPMASATHYCYTNHVLISGCRDHSHQVALGVL-----RTTANGRIFFSTLASI 227
Db 3048 LIIPFTFNITNLHAYEENMQHPSRKRTTERVLQ-GLKPLFKNTSVGL-YSGCRLT 3105
Qy 228 SLDDTQ-----NRKCSVSATPLGDM-LCSKYTEEEDYNASAPTIM 270
Db 3106 SLRPEKDAATGMADVCLYHNPKRPGIDRQGLWELSQGLTINITELG-----PSTL 3157
Qy 271 AHGRLGPDQYHEKDLVTTLFEDWVANYPGVGGSFIDGRVWFSVYGLKPNSPDVTQ 330
Db 3158 DRDSLIVNGFTHONSVPPTST-----PGT-----STVYMATG-TPSSPFGHTE 3200
Qy 331 EGKVIYKRYNDTCDEDDQYQIRMAKSSYKPG-RFG-GKRIQOAILG-IKVSTSLG- 384
Db 3201 PGLPIIPFTFNITN-----LHAYEENMQHPSRKRTTERVLQGLKPLFKNTSVGLY 3255
Qy 385 -----DPV-----LTVPNTVTLMGABGRIL 405
Db 3256 SGCRIILRPEKHAATGVDITCTHRVDPISGDLRKLWELSQGLTINITELG----- 3310
Qy 406 TVGTSHPLYORGSY--FSPALYPMVSNKTATLHSPYFNAPTRPGSIPCOASACP 462
Db 3311 -----YTLDRDSLIVNGFNPSSVPTSTPGSTVHLATSGTPSLPG----- 3353
Qy 463 NSCVTVGVTDPYPLI--FYRNHTLAGVFGTMDSQOALNPASVFDSTSR 511
Db 3354 -----HTAPVPLIIPFTLNFTI-----TNLHAYEENMQHPSRKRTTER 3392

```

RESULT 12

```

US-09-738-626-3707
; Sequence 3707, Application US/09738626
; Publication No. US20020197605A1
; GENERAL INFORMATION:
; APPLICANT: NAKAGAMA, SATOSHI
; APPLICANT: MIZOGUCHI, HIROSHI
; APPLICANT: ANDO, SEIKO
; APPLICANT: HAYASHI, MIKIRO
; APPLICANT: OCHIAI, KEIKO
; APPLICANT: YOKOI, HARUHIKO
; APPLICANT: TATEISHI, NAOKO
; APPLICANT: SENOH, AKIHIRO
; APPLICANT: IKEDA, MASATO
; APPLICANT: OZAKI, AKIO
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-125
; CURRENT APPLICATION NUMBER: US/09/738, 626
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: JP 99/377484
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: JP 00/280988
; PRIOR FILING DATE: 2000-08-03
; NUMBER OF SEQ ID NOS: 7059
; SOFTWARE: PatentIn ver. 3.0
; SEQ ID NO 3707
; LENGTH: 1510
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-09-738-626-3707

```

Query Match 3.7%; Score 109.5; DB 10; Length 1510;

```

Best Local Similarity 20.1%; Pred. No. 0.77;
Matches 99; Conservative 63; Mismatches 181; Indels 149; Gaps 24;
Qy 47 SMGASTSDU-----VGIPTRISRAEKITSALGSDQDV-----DRIYQVALLSPAL 96
Db 576 SFGNAVISGLYPAVHAGMKAIAIARVREVESEAIRNGKITLIYUSDESBERMAPIPALL 635
Qy 97 L-----NTETTMAITS-LSYOINGAANNNGMGAIPHDPFI-----G 134
Db 636 LTSAVHGYLVQQRRTQCSLVESGDAREVHMLMLGFGADAINPVAPEITDELHAKG 695
Qy 135 GIGKELIYDNAS-----DVTSPFSAFOEHLNF 162
Db 696 QLG-DLSIDEASRYIKAATTVGLKWSKMGIAVSSYRGAQLADVGLHQDLIDNYFGG 754
Qy 163 IPAPTTSGCRRISFPMASATHYCYTNHVLISGCRDHSHQVALG----- 209
Db 755 IASPISGIGLDEVA--DVEARH-----RSAPLP--RPEHAREIDLQGEYKMRREGEVHL 807
Qy 210 -----VLTPTATG--RIFFSTLRISLDDTONRKSQVSATPLGCDMLCSKYETEE 259
Db 808 FNPETIFRLOHATSSGSEYEIFKDYTRKY--DDOSTRLGTIRGLFEPSTDRKPIVSSEVP 865
Qy 260 EDYNSAVPTLMAHGRIGPDQYHEKDLVTTLFEDWVANYPGVGGSFIDGRVWFSVYGG 319
Db 866 V---SEIVKRFSTGAMSY-GSISAHEVLIANNRILGMSNSGEGG-EDARRF-----D 915
Qy 320 LKPN-----SPSDVVOGKVIYKRYNDTCDEDDQYQIRMAKSSYKRGFKRIQOAIL 374
Db 916 VEPNGDMKRSIAIKOVASGRFQVSHYLNLC--TDIOIKAOQA-KPGE-QGQ----- 963
Qy 375 SIKVSTSLGSDPVLTPPNTVTLMGABGRILTVGTS-----HFLYORGSYSPALLY 427
Db 964 -----LFPNKVYPMVAEVRITTBVGSLSPPHHDYI-----SIEDLAQLIH 1005
Qy 428 PMTVSNKTATLH 439
Db 1006 DLKANPRAARIH 1017

```

RESULT 13

```

US-10-369-493-1535
; Sequence 1535, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369, 493
; PRIOR FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360, 039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 1535
; LENGTH: 1609
; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
US-10-369-493-1535

```

Query Match 3.6%; Score 108; DB 12; Length 1609;  
 Best Local Similarity 19.4%; Pred. No. 1.2;  
 Matches 123; Conservative 79; Mismatches 227; Indels 206; Gaps 23;

```

Qy 30 LLLTVVTLATSVASIVSMGASTSDLVGIPTRISRAEKITSALGSDQDVRIYQV- 88
Db 748 LVLSVTVTYVNGAATETTYWC--PASSIAVYTSISYTLVLTVEVCHSSECTPTVITSVT 805
Qy 89 ALBSPALALNTETTMAITSLSYOINGAANNNGMGAIPHDPFGIGKELIYDNASDV 148

```

Db 806 ATSTTIPLLSTSSS-----TVLSSTVEGAKN----- 832  
Qy 149 TSPFPAFQEHLPNIPAPTTGSGCTRIAPSPDMKTHCYTHNVLSCGRHSHQYIAL 208  
Db 833 -----PAASEVTINTQVATSEARST-----STQVATATATAASSSTTSQVSTSETITSL 885  
Qy 209 GVLRTATGRIFPFTLSISLDDT--ONRKSQVSATPLGCDMLCSKYTEEDDYNASVP 267  
Db 886 GTQNFPTTGLPLPALSTEMINTTVSRKLIIS-----TEVCSHAKCVP 930  
Qy 268 TLMAH--GRLGFGQYHEKD-----LDVTTLFEDWVANYPGVGGGPFIDGRWFVSV-- 316  
Db 931 TVITEVVTSGTSPNGHSSQTLQTEAVEVTLSSHQVTVMTSEVCSNICTPVTITSVQMR 990  
Qy 317 ----YGLKPNSPSTVEGKVIYKRYND-----TCDEDDYQIRMAKSS 358  
Db 991 STEPPYLTSTSSSLASTKSSLEASSESTSPSTQSLPLFTCSER-----RST 1042  
Qy 359 YKGRFGGRKIQQAISIKVST--SLGEDPVLTVPPNTVTLMGAGRILTVGTSHFLYQRG 417  
Db 1043 TSVSQMNTVLTNTIMSSSNVISTNEKPSSTSP-----YNFS 1081  
Qy 418 SSYFSPALLYPMTVSNKTAI-----LHSPYT-----FNAFTR 449  
Db 1082 SGYSLPSSSTPSQVSLSTATTTTNGIKTVYTTWCPLAKSTVAASSQSSRSDVRPVSXK 1141  
Qy 450 PGSLPCQASARCPNSCTY-----GYTDPYPLIFRNTLKGVCFTMDSEQARLNP 502  
Db 1142 PSSSLSGTSTIQYTLSTATTITISGLKTYVTTWCPL-----TSKSTLG-----A 1183  
Qy 503 SAVDSTSRSRITRVS--SSTKAAVTTST-----CFKVVTKNTK-- 540  
Db 1184 TTQSTSTAKYRITRASSATSTISLSSTSESSSGYLSKGVCSGTCTQDVPFQSSSPA 1243  
Qy 541 ----YCLISIAEIS-----NTLFGEFRIVPL 562  
Db 1244 STLAYSPTSVSTSSSSFSSTTASTLTSTHTSVPL 1278

RESULT 14  
US-10-032-189-128  
Sequence 128, Application US/10032189  
Publication No.: US20030170630A1  
GENERAL INFORMATION:  
APPLICANT: Alsobrook II, John P  
APPLICANT: Tchernev, Velizar T  
APPLICANT: Liu, Xiaohong  
APPLICANT: Spytek, Kimberly A  
APPLICANT: Zehrhusen, Bryan D  
APPLICANT: Patturajan, Meera  
APPLICANT: Grosee, William M  
APPLICANT: Lepley, Denise M  
APPLICANT: Burgess, Catherine E  
APPLICANT: Shinkets, Richard A  
APPLICANT: Grosee, William M  
APPLICANT: Szekeres, Edward S  
APPLICANT: Vernet, Corine A.M.  
APPLICANT: Li, Li  
APPLICANT: Casman, Stacie J  
APPLICANT: Boldog, Ferenc L  
APPLICANT: Gorman, Linda  
APPLICANT: Gangoli, Beba A  
APPLICANT: Fernandes, Elma R  
APPLICANT: Rieger, Daniel K  
APPLICANT: Edinger, Shlomit R  
APPLICANT: Gunther, Erik  
APPLICANT: Miller, Isabelle  
APPLICANT: Sciore, Paul  
APPLICANT: Ellerman, Karen  
APPLICANT: Macdougall, John R  
APPLICANT: Smithson, Glenda  
TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same

FILE REFERENCE: 21402-228  
CURRENT APPLICATION NUMBER: US/10/032,189  
CURRENT FILING DATE: 2001-12-21  
PRIOR APPLICATION NUMBER: 60/257,495  
PRIOR FILING DATE: 2000-12-21  
PRIOR APPLICATION NUMBER: 60/258,171  
PRIOR FILING DATE: 2000-12-20  
PRIOR APPLICATION NUMBER: 60/269,940  
PRIOR FILING DATE: 2001-02-20  
PRIOR APPLICATION NUMBER: 60/274,192  
PRIOR FILING DATE: 2001-03-08  
PRIOR APPLICATION NUMBER: 60/277,826  
PRIOR FILING DATE: 2001-03-22  
PRIOR APPLICATION NUMBER: 60/279,840  
PRIOR FILING DATE: 2001-03-29  
PRIOR APPLICATION NUMBER: 60/282,981  
PRIOR FILING DATE: 2001-04-11  
PRIOR APPLICATION NUMBER: 60/283,656  
PRIOR FILING DATE: 2001-04-13  
PRIOR APPLICATION NUMBER: 60/309,247  
PRIOR FILING DATE: 2001-07-31  
PRIOR APPLICATION NUMBER: 60/311,754  
PRIOR FILING DATE: 2001-08-17  
PRIOR APPLICATION NUMBER: 60/313,331  
PRIOR FILING DATE: 2001-08-17  
NUMBER OF SEQ ID NOS: 260  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 128  
LENGTH: 5636  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: VARIANT  
LOCATION: (3003)  
OTHER INFORMATION: wherein Xaa is any amino acid.  
FEATURE:  
NAME/KEY: VARIANT  
LOCATION: (3041)  
OTHER INFORMATION: wherein Xaa is any amino acid.  
FEATURE:  
NAME/KEY: VARIANT  
LOCATION: (3367)  
OTHER INFORMATION: wherein Xaa is any amino acid.  
US-10-032-189-128

Query Match 3.6%; Score 108; DB 12; Length 5636;

Best Local Similarity 21.8%; Pred. No. 9.5; Indels 184; Gaps 35;

Matches 131; Conservative 65; Mismatches 221; Indels 184; Gaps 35;

Qy 20 TWRLPRIALILLTVVTLATSVASLVYSGASTPSDVLGIPRISRABE--KITSALGSN 77  
Db 3 SWEVHTVFLFALLISSLA-----ODASPOSEI-----RAEFPPGASTLAV 45  
Qy 78 ODVDRIVKQV--ALSPALANTETTNNATTSLSYQINGAANSGWGAPIHDPDFIG 135  
Db 46 FQVTSMDVDDIVQVEGASKIL--ETSLKRPKRP--FNPL-----VPRHDP 90  
Qy 136 ICKELIVNASDVTSTYPSAFQEHLPNFI-----PAFTGSGCTRI--SF----- 178  
Db 91 IGPVITITD-----PKFQYELRELVYGGGDCPEMSIAIKALEISLPGSFIYV 142  
Qy 179 -DMSATHYCYTHNV-----ILSG--CRDHSHQYIALGVLTATNGRIFF-- 221  
Db 143 TDARKSDVRLTHEVLOLIQKOSQVVFVLTGCDDBRTH--GKYVYEIASSSTSGQVFIHD 201  
Qy 222 -----STLRSISLDDTGNRKSQVSATPLGCDMLCSKYTEEDDYNAS 264  
Db 202 KKQVNEVLKWEAVQASVHLSTDHLEQ---AVNTWRIFPDSLKKEVT-----VSL 251  
Qy 265 AVPTLMAH-----GRV-----GPDQYHE-----KDDVTTLFED-----WYANPGV 303  
Db 252 SGSPMIEIRNPLGKLIKKGFG--LHELLHNHSAKVNVKPEAGMWTVKTSSSGRHSV 309

QY 304 ---GGSFIDGRWSEVYGLK-----NSPSDTYQF-GKVIYIKRYNDTCPEBODY--QI 352  
 Db 310 RTGLSTIDFRAGFS-----RKPTLDFKTVSRVQGIPTVVLINTSGISTPARIDLEL 365  
 QY 353 RMAKSSYK--PGRFGKRIQQAIIISIKVSTSLGDEPVLTVPPNTVTLMGAEGRILTVGS 410  
 Db 366 SISGSSSLKTIPIVKYIYHRRKPYGIWNIISD-----FVPPNEAFELKVTG---YDKD 411  
 QY 411 HFLYORGSSYFSPALLYP---MTVSNKTATLHSPYFNAPTRPGSIPCOASARCPNSCV 466  
 Db 412 DYLFQGVSS--VSFSSIVDPAPKVTMEKTP-----GYILOPQOIPCSVDLSL----- 457  
 QY 467 TGVYTDYPLIFRYRNHTLRCVFGTMDSEQARLNPAFAVDFSTSRRTTRVSSSSSTKAY 526  
 Db 458 -----PFTLSFVRNGVTLGVDOYLKESASVSLIDIAKVTLSDEGFYECIAVSSAGTGRAQ 511  
 QY 527 T 527  
 Db 512 T 512

RESULT 15

US-10-120-801-72

Sequence 72, Application US/10120801

Publication No. US20030203843A1

GENERAL INFORMATION:

APPLICANT: Pena, Carol

APPLICANT: Guo, Xiaojia

APPLICANT: Shimkets, Richard

APPLICANT: Padigaru, Muralidhara

APPLICANT: Kerkuda, Ramesh

APPLICANT: Spytek, Kimberly

APPLICANT: Mehraban, Foad

APPLICANT: Topper, James N.

APPLICANT: Malyankar, Uriel

APPLICANT: Wasserman, Scott

APPLICANT: Edinger, Shlomit

APPLICANT: Smithson, Glennda

APPLICANT: Gunther, Erik

APPLICANT: Komuves, Laszlo

TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same

FILE REFERENCE: 21402-140

CURRENT APPLICATION NUMBER: US/10/120,801

CURRENT FILING DATE: 2002-04-11

PRIOR APPLICATION NUMBER: 60/285748

PRIOR FILING DATE: 2001-04-23

PRIOR APPLICATION NUMBER: 60/286068

PRIOR FILING DATE: 2001-04-24

PRIOR APPLICATION NUMBER: 60/286292

PRIOR FILING DATE: 2001-04-25

PRIOR APPLICATION NUMBER: 60/288334

PRIOR FILING DATE: 2001-05-03

PRIOR APPLICATION NUMBER: 60/291241

PRIOR FILING DATE: 2001-05-16

PRIOR APPLICATION NUMBER: 60/322284

PRIOR FILING DATE: 2001-09-14

PRIOR APPLICATION NUMBER: 60/285609

PRIOR FILING DATE: 2001-04-20

NUMBER OF SEQ ID NOS: 155

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 72

LENGTH: 5636

TYPE: PRT

ORGANISM: human

FEATURE:

NAME/KEY: VARIANT

LOCATION: (3003)

OTHER INFORMATION: wherein Xaa is any amino acid.

NAME/KEY: VARIANT

LOCATION: (3041)

OTHER INFORMATION: wherein Xaa is any amino acid.

FEATURE:

NAME/KEY: VARIANT  
 LOCATION: (3367)  
 OTHER INFORMATION: wherein Xaa is any amino acid.  
 US-10-120-801-72

Query Match 3.6%; Score 108; DB 12; Length 5636;  
 Best Local Similarity 21.8%; Pred. No. 9.5;  
 Matches 131; Conservative 65; Mismatches 221; Indels 184; Gaps 35.

QY 20 TWRLIFRAIILLVYVTLATISVASLYSMGASTSDVLGIPTRISRAEE--KITSALGSN 77  
 Db 3 SMEVHTVFLPALYSSIA-----QDASPOSEI-----RAEEFEGASTLAFAV 45  
 QY 78 ODVDRIYKQV--ALESPALNTETITMAITSLVSQINGAANNMGCAIHPDPFG 135  
 Db 46 FDTGSMYDDLVQVYEGASKTL--ETSLKRPKRL--FNAL-----VFHDPE--- 90  
 QY 136 IGKELVDNADSVTSFYSAFOEHLNFI-----PAPYSGCTRIIP-----SF----- 178  
 Db 91 IGPVITITD-----PKKQYELRELYVGGGDCPEMSGAIKIALEISLPGSFYVF 142  
 QY 179 -DMSATHCYTHNV-----ILSG-CRDHSHQYALGVLRITATGRIFP-- 221  
 Db 143 TDARSKDYRLTHEVLIQIQKQSOVFLTGDCDDBRTHI--GYKYEEIATSSGQVPHLD 201  
 QY 222 -----STLRSLDDTONRKSGSVSATPLGCDMLCSKYTETEEDYNS 264  
 Db 202 KKQVNEVLKAVEEVAQSKVHLSTDLQO-----AVNTWRIIPFQSLKEVT-----VSL 251  
 QY 265 AVPTLMAN-----GRL--GFDQYHE-----KDLDTTLFED-----MVANYPGVG--- 303  
 Db 252 SGSPFMIEINPLGKLIKGGFG--LHLLNHNHSAKVNVKPEPAGMWYTKTSSGHSV 309  
 QY 304 ---GGSFIDGRWSEVYGLK-----NSPSDTYQF-GKVIYIKRYNDTCPEBODY--QI 352  
 Db 310 RTGLSTIDFRAGFS-----RKPTLDFKTVSRVQGIPTVVLINTSGISTPARIDLEL 365  
 QY 353 RMAKSSYK--PGRFGKRIQQAIIISIKVSTSLGDEPVLTVPPNTVTLMGAEGRILTVGS 410  
 Db 366 SISGSSSLKTIPIVKYIYHRRKPYGIWNIISD-----FVPPNEAFELKVTG---YDKD 411  
 QY 411 HFLYORGSSYFSPALLYP---MTVSNKTATLHSPYFNAPTRPGSIPCOASARCPNSCV 466  
 Db 412 DYLFQGVSS--VSFSSIVDPAPKVTMEKTP-----GYILOPQOIPCSVDLSL----- 457  
 QY 467 TGVYTDYPLIFRYRNHTLRCVFGTMDSEQARLNPAFAVDFSTSRRTTRVSSSSSTKAY 526  
 Db 458 -----PFTLSFVRNGVTLGVDOYLKESASVSLIDIAKVTLSDEGFYECIAVSSAGTGRAQ 511  
 QY 527 T 527  
 Db 512 T 512

Search completed: January 2, 2004, 16:25:03  
 Job time : 54 secs

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